ATTN: Ed Hurt.

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ACCESS DB # 165067

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Scientific and Technical Information Center

CRF

SEARCH REQUEST FORM

Requester's Full Name: Celine Qian Examiner #: (STIC) 78770 Date: 9/7/05

Art Unit: 1636 Phone Number: 2- 0777 Serial Number: 10/030658

Location (Bldg/Room#): 7A64 (Mailbox #): 2C70 Results Format Preferred (circle): PAPER DISK

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following: MG

Title of Invention: Trap vectors and gene trapping meth. by using the sam

Inventors (please provide full names): Yamamura et al.

Earliest Priority Date: 7/14/1999

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search SEQ ID NO: 15 and SEQ ID NO: 16.

****

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Searcher: _____

Searcher Phone #: _____

Searcher Location: _____

Date Searcher Picked Up: 9/8/05

Date Completed: 9/9/05

Searcher Prep & Review Time: _____

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Type of Search

X NA Sequence (#)

_____ AA Sequence (#)

_____ Structure (#)

_____ Bibliographic

_____ Litigation

_____ Fulltext

_____ Other

Vendors and cost where applicable

_____ STN _____ Dialog

_____ Questel/Orbit _____ Lexis/Nexis

_____ Westlaw _____ WWW/Internet

X In-house sequence systems

X Commercial ___ Oligomer ___ Score/Length

X Interference ___ SPDI ___ Encode/Transl

_____ Other (specify)

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STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 156067

TO: Celine Qian
Location: rem/2A64/2C70
Art Unit: 1636
Friday, September 09, 2005

Case Serial Number: 10/030658

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact ***the searcher or contact:***

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

- *I am an examiner in Workgroup:* ☐ *Example: 1610*
- *Relevant prior art **found**, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
  (journal articles, conference proceedings, new product announcements etc.)

- *Relevant prior art **not found:***
  - ☐ Results verified the lack of relevant prior art (helped determine patentability).
  - ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC Biotech-Chem Library, Remsen Bldg

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 21:11:18 ; Search time 797 Seconds
(without alignments)
2067.098 Million cell updates/sec

Title: US-10-030-658B-15
Perfect score: 34
Sequence: 1 taccgttcgtatagcatacattatacgaagttat 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	34	100.0	34	6	BD182868	BD182868 Knockout
	2	34	100.0	34	6	BD185622	BD185622 Knockout
	3	34	100.0	34	6	AX114843	AX114843 Sequence
	4	34	100.0	34	6	AX137069	AX137069 Sequence
c	5	34	100.0	34	6	AX540640	AX540640 Sequence
	6	34	100.0	34	6	AX710009	AX710009 Sequence
	7	34	100.0	34	6	AX710011	AX710011 Sequence
	8	34	100.0	34	6	BD083072	BD083072 Antisense
	9	34	100.0	34	6	BD093611	BD093611 Antisense
	10	34	100.0	44	6	AX710018	AX710018 Sequence
	11	34	100.0	68	6	AX710014	AX710014 Sequence
c	12	34	100.0	78	6	AX114851	AX114851 Sequence
	13	34	100.0	79	6	AX114852	AX114852 Sequence
	14	34	100.0	94	6	AX662254	AX662254 Sequence
	15	34	100.0	94	6	AX662260	AX662260 Sequence
c	16	34	100.0	5054	6	BD083076	BD083076 Antisense
c	17	34	100.0	5054	6	BD093615	BD093615 Antisense
c	18	34	100.0	7175	6	AX114853	AX114853 Sequence
c	19	34	100.0	8153	6	AX114871	AX114871 Sequence
	20	34	100.0	8811	12	AY569779	AY569779 Cloning v
	21	34	100.0	9479	12	AY569778	AY569778 Cloning v
	22	34	100.0	12404	12	AY569780	AY569780 Cloning v
	23	32.4	95.3	34	6	AX710010	AX710010 Sequence
	24	30.8	90.6	34	6	AX710012	AX710012 Sequence
c	25	30.8	90.6	10695	12	AY553053	AY553053 Reporter
c	26	30.8	90.6	53099	2	AC101086	AC101086 Mus muscu
c	27	30.8	90.6	64634	2	AC100010	AC100010 Mus muscu
	28	30.4	89.4	65346	2	AC026597	AC026597 Homo sapi
c	29	30.4	89.4	71199	2	AC074079	AC074079 Homo sapi
	30	30.4	89.4	74315	2	AC023029	AC023029 Homo sapi
c	31	30.4	89.4	80363	2	AC025805	AC025805 Homo sapi
	32	30.4	89.4	87939	2	AC021740	AC021740 Homo sapi
c	33	30	88.2	68581	2	AC027375	AC027375 Homo sapi
	34	29.8	87.6	41871	2	CEH27D13	Z92798 Caenorhabdi
c	35	29.8	87.6	70835	2	AC116388	AC116388 Homo sapi
c	36	29.4	86.5	51500	2	AC100461	AC100461 Mus muscu
c	37	29.4	86.5	64036	2	AC040921	AC040921 Homo sapi
c	38	29.4	86.5	70984	2	AC068078	AC068078 Homo sapi
c	39	29.4	86.5	81967	2	AC139069	AC139069 Homo sapi
c	40	29.4	86.5	85186	2	AC021348	AC021348 Homo sapi
c	41	29.4	86.5	89044	2	AC022633	AC022633 Homo sapi
c	42	29.4	86.5	89221	2	AC138746	AC138746 Homo sapi
c	43	29.4	86.5	276475	2	AC109180	AC109180 Mus muscu
	44	29.2	85.9	55787	2	AC090406	AC090406 Homo sapi
c	45	29.2	85.9	57858	2	AC087572	AC087572 Homo sapi

ALIGNMENTS

RESULT 1
BD182868
LOCUS BD182868 34 bp DNA linear PAT 17-JUN-2003
DEFINITION Knockout animal.
ACCESSION BD182868
VERSION BD182868.1 GI:31875068
KEYWORDS JP 2002345477-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 34)
AUTHORS Ide,H., Yamamura,K. and Araki,K.
TITLE Knockout animal
JOURNAL Patent: JP 2002345477-A 1 03-DEC-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
KIMI ARAKI
COMMENT OS Artificial Sequence
PN JP 2002345477-A/1
PD 03-DEC-2002
PF 25-MAY-2001 JP 2001157567
PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
Description of Artificial Sequence:synthetic DNA FH Key
Location/Qualifiers
FT source 1. .34
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .34
/organism="synthetic construct"
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ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

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RESULT 2
BD185622
LOCUS       BD185622                  34 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Knockout animal.
ACCESSION   BD185622
VERSION     BD185622.1  GI:31877822
KEYWORDS    JP 2002369689-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Ide,H., Yamamura,K. and Araki,K.
  TITLE     Knockout animal
  JOURNAL   Patent: JP 2002369689-A 1 24-DEC-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
            KUMAMOTO UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002369689-A/1
            PD   24-DEC-2002
            PF   25-MAY-2001 JP 2001157568
            PI   HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
            PC   C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
            Description of Artificial Sequence:synthetic DNA FH   Key
              Location/Qualifiers
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FEATURES              Location/Qualifiers
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ORIGIN

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  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 3
AX114843
LOCUS       AX114843                  34 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 3 from Patent WO0129208.
ACCESSION   AX114843
VERSION     AX114843.1  GI:14031785
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 3 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES              Location/Qualifiers
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ORIGIN

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              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 4
AX137069
LOCUS       AX137069                  34 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 3 from Patent EP1092768.
ACCESSION   AX137069
VERSION     AX137069.1  GI:14273414
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R. and von Melchner,H.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: EP 1092768-A 3 18-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; FrankGen Biotechnologie AG (DE)
FEATURES              Location/Qualifiers
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                      /note="mutant loxP site - lox71"
ORIGIN

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Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 5
AX540640/c
LOCUS       AX540640                  34 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 9 from Patent WO0240685.
ACCESSION   AX540640
VERSION     AX540640.1  GI:25273628
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Xin,H.B. and Kotlikoff,M.
  TITLE     Vectors for conditional gene inactivation
  JOURNAL   Patent: WO 0240685-A 9 23-MAY-2002;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES              Location/Qualifiers
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ORIGIN

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Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 6
AX710009
LOCUS       AX710009                  34 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from Patent EP1288295.
ACCESSION   AX710009
VERSION     AX710009.1  GI:29786620
KEYWORDS    .
SOURCE      synthetic construct
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  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Altmann,M., Neuhierl,B. and Hammerschmidt,W.
  TITLE     Use of mutated recognition sites for multiple successive recombina
            se-mediated recombinations in a genetic system
  JOURNAL   Patent: EP 1288295-A 6 05-MAR-2003;
            GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
FEATURES             Location/Qualifiers
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                     /note="Oligonukleotid lox 71 ohne flanks"
ORIGIN

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  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 7
AX710011
LOCUS       AX710011                  34 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from Patent EP1288295.
ACCESSION   AX710011
VERSION     AX710011.1  GI:29786622
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Altmann,M., Neuhierl,B. and Hammerschmidt,W.
  TITLE     Use of mutated recognition sites for multiple successive recombina
            se-mediated recombinations in a genetic system
  JOURNAL   Patent: EP 1288295-A 8 05-MAR-2003;
            GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 8
BD083072
LOCUS       BD083072                  34 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense type gene trap vector.
ACCESSION   BD083072
VERSION     BD083072.1  GI:22628682
KEYWORDS    JP 2001321174-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Taniguchi,K. and Karasawa,M.
  TITLE     Antisense type gene trap vector
  JOURNAL   Patent: JP 2001321174-A 2 20-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2001321174-A/2
            PD   20-NOV-2001
            PF   11-MAY-2000 JP 2000138938
            PI   KATSUMI TANIGUCHI,MIKA KARASAWA
            PC   C12N15/09,A01K67/027,C12N5/10//(C12N5/10,C12R1:91),C12N15/00,
            PC   C12N5/00,
            PC   (C12N5/00,C12R1:91)
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Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 9
BD093611
LOCUS       BD093611                  34 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense gene trap vector.
ACCESSION   BD093611
VERSION     BD093611.1  GI:22639199
KEYWORDS    WO 0185973-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Taniguchi,M. and Karasawa,M.
  TITLE     Antisense gene trap vector
  JOURNAL   Patent: WO 0185973-A 2 15-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP,MASARU TANIGUCHI,MIKA KARASAWA
COMMENT     OS   Artificial Sequence
            PN   WO 0185973-A/2
            PD   15-NOV-2001
            PF   29-AUG-2000 WO 2000JP005824
            PR   11-MAY-2000 JP 00P   138938
            PI   MASARU TANIGUCHI,MIKA KARASAWA
            PC   C12N15/85,C12N5/10,A01K67/027//A61K48/00
            CC   Description of Artificial Sequence:lox71 sequence FH   Key
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
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RESULT 10
AX710018
LOCUS       AX710018                  44 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 15 from Patent EP1288295.
ACCESSION   AX710018
VERSION     AX710018.1  GI:29786629
KEYWORDS    .
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Altmann,M., Neuhierl,B. and Hammerschmidt,W.
  TITLE     Use of mutated recognition sites for multiple successive recombina
            se-mediated recombinations in a genetic system
  JOURNAL   Patent: EP 1288295-A 15 05-MAR-2003;
            GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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RESULT 11
AX710014
LOCUS       AX710014                  68 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 11 from Patent EP1288295.
ACCESSION   AX710014
VERSION     AX710014.1  GI:29786625
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Altmann,M., Neuhierl,B. and Hammerschmidt,W.
  TITLE     Use of mutated recognition sites for multiple successive recombina
            se-mediated recombinations in a genetic system
  JOURNAL   Patent: EP 1288295-A 11 05-MAR-2003;
            GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         11 TACCGTTCGTATAGCATACATTATACGAAGTTAT 44


RESULT 12
AX114851/c
LOCUS       AX114851                  78 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 11 from Patent WO0129208.
ACCESSION   AX114851
VERSION     AX114851.1  GI:14031793
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 11 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .78
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer lox3"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         78 TACCGTTCGTATAGCATACATTATACGAAGTTAT 45


RESULT 13
AX114852
LOCUS       AX114852                  79 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 12 from Patent WO0129208.
ACCESSION   AX114852
VERSION     AX114852.1  GI:14031794
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 12 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .79
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer lox4"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39


RESULT 14
AX662254
LOCUS       AX662254                  94 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 10 from Patent WO02083889.
ACCESSION   AX662254
VERSION     AX662254.1  GI:29163153
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bigger,B.W., Tolmachov,O. and Coutelle,C.
  TITLE     Methods
  JOURNAL   Patent: WO 02083889-A 10 24-OCT-2002;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .94
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
ORIGIN
```

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  Best Local Similarity  100.0%;  Pred. No. 0.015;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83


RESULT 15
AX662260
LOCUS       AX662260                  94 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 16 from Patent WO02083889.
ACCESSION   AX662260
VERSION     AX662260.1  GI:29163159
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bigger,B.W., Tolmachov,O. and Coutelle,C.
  TITLE     Methods
  JOURNAL   Patent: WO 02083889-A 16 24-OCT-2002;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .94
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
ORIGIN

  Query Match            100.0%;  Score 34;  DB 6;  Length 94;
  Best Local Similarity  100.0%;  Pred. No. 0.015;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 21:09:03 ; Search time 200.5 Seconds
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Title: US-10-030-658B-15
Perfect score: 34
Sequence: 1 taccgttcgtatagcatacattatacgaagttat 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		34	100.0	34	5	AAD04917	Aad04917 Recombina
c 2		34	100.0	34	6	ABN84175	Abn84175 LoxP left
3		34	100.0	34	6	ABA03775	Aba03775 Synthetic
4		34	100.0	34	8	ABZ20929	Abz20929 LoxP muta
5		34	100.0	34	8	ABZ20931	Abz20931 LoxP muta
6		34	100.0	34	8	ABZ79444	Abz79444 Lox 71 DN
7		34	100.0	34	9	ACC85309	Acc85309 Recombina
c 8		34	100.0	34	10	ADD13802	Add13802 Oligonucl
9		34	100.0	34	10	ADD15151	Add15151 Variant l
10		34	100.0	34	10	ABZ75319	Abz75319 Lox71 rel
11		34	100.0	44	8	ABZ20936	Abz20936 Lox71 iso
12		34	100.0	68	8	ABZ20922	Abz20922 Lox66 and
c 13		34	100.0	78	5	AAD04925	Aad04925 Primer lo
14		34	100.0	79	5	AAD04926	Aad04926 Primer lo
15		34	100.0	94	8	ABV75994	Abv75994 OLIGO-F,
16		34	100.0	94	8	ABV75989	Abv75989 Oligonucl
c 17		34	100.0	5054	6	ABA03779	Aba03779 Gene trap
c 18		34	100.0	7175	5	AAD04927	Aad04927 Vector pR
c 19		34	100.0	8153	5	AAD04945	Aad04945 Plasmid p
20		32.4	95.3	34	8	ABZ20930	Abz20930 LoxP muta
c 21		31	91.2	63	2	AAT61668	Aat61668 Chloramph
22		30.8	90.6	34	8	ABZ20932	Abz20932 LoxP muta
23		30.8	90.6	34	9	ACC85311	Acc85311 Recombina
24		29	85.3	32	5	AAC92431	Aac92431 Lox P sit
25		29	85.3	32	10	ADE52399	Ade52399 LoxP site
c 26		29	85.3	34	2	AAQ47238	Aaq47238 loxP sequ
27		29	85.3	34	2	AAQ47239	Aaq47239 loxP sequ
c 28		29	85.3	34	2	AAQ94929	Aaq94929 Wild type
c 29		29	85.3	34	2	AAT42299	Aat42299 Bacteriop
30		29	85.3	34	2	AAT36911	Aat36911 E. coli p
c 31		29	85.3	34	2	AAT92195	Aat92195 Bacteriop
c 32		29	85.3	34	2	AAT90585	Aat90585 Lox p rec
c 33		29	85.3	34	2	AAV17069	Aav17069 Lox P1 se
c 34		29	85.3	34	2	AAX76189	Aax76189 Variant l
c 35		29	85.3	34	2	AAX61038	Aax61038 Yeast Lox
36		29	85.3	34	2	AAX76039	Aax76039 5' to 3'
37		29	85.3	34	2	AAX19902	Aax19902 Wild-type
38		29	85.3	34	3	AAA58294	Aaa58294 Bacteriop
c 39		29	85.3	34	3	AAA58293	Aaa58293 Bacteriop
40		29	85.3	34	3	AAZ58066	Aaz58066 Wild-type
c 41		29	85.3	34	3	AAA91994	Aaa91994 Insert re
c 42		29	85.3	34	3	AAA10908	Aaa10908 Lox site
43		29	85.3	34	3	AAA10911	Aaa10911 Lox P sit
44		29	85.3	34	3	AAC61510	Aac61510 Nucleotid
45		29	85.3	34	3	AAA10234	Aaa10234 Bacteriop

ALIGNMENTS

RESULT 1
AAD04917
ID AAD04917 standard; DNA; 34 BP.
XX
AC AAD04917;
XX
DT 17-JUL-2001 (first entry)
XX
DE Recombinase recognition sequence (RRS), loxP site mutant (lox71) DNA.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; loxP site; mutant; ds.
XX
OS Enterobacteria phage P1.
OS Synthetic.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-EP010162.
XX
PR 16-OCT-1999; 99EP-00120592.
PR 27-OCT-1999; 99US-0162016P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI Kuehn R, Von Melchener H, Altschmied J;
XX
DR WPI; 2001-308486/32.
XX
PT New gene trapping construct capable of causing conditional mutations in
PT genes, comprises functional DNA segment inserted in sense or antisense
PT direction relative to gene to be trapped.
XX
PS Claim 4; Page 49; 78pp; English.
XX
CC The present invention relates to a conditional gene trapping construct
CC capable of causing conditional mutations in genes. The gene trapping
CC construct comprises two functional DNA segments, each being flanked by
CC two recombinase recognition sequences (RRSs) specific to site specific

```
CC   recombinase which is capable of unidirectional inversion of double
CC   standard DNA segment. One of the DNA segment (disruption cassette) is
CC   inserted in antisense orientation relative to the transcriptional
CC   orientation of the gene to be trapped. The other DNA segment (selection
CC   cassette) is inserted in sense direction relative to the transcriptional
CC   orientation of the gene to be trapped. The cell comprising the gene
CC   trapping construct is useful for the identification and/or isolation of
CC   genes. The transgenic organism comprising the gene trapping construct is
CC   useful to study gene function at various developmental stages. The gene
CC   trapping construct is useful for mutationally inactivating all cellular
CC   genes. The present DNA sequence encodes recombinase recognition sequence,
CC   loxP site mutant (lox71), which flanks the functional DNA segments of
CC   gene trapping construct
XX
SQ   Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 2
ABN84175/c
ID   ABN84175 standard; DNA; 34 BP.
XX
AC   ABN84175;
XX
DT   23-SEP-2002  (first entry)
XX
DE   LoxP left element mutant.
XX
KW   Gene inactivation; mutagenesis; vector; knockout animal;
KW   transgenic animal; gene trapping; loxP; mutant; ss.
XX
OS   Enterobacteria phage P1.
OS   Synthetic.
XX
PN   WO200240685-A2.
XX
PD   23-MAY-2002.
XX
PF   16-NOV-2001; 2001WO-US043916.
XX
PR   16-NOV-2000; 2000US-0249200P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Xin H,  Kotlikoff M;
XX
DR   WPI; 2002-537342/57.
XX
PT   Novel genetically engineered vector comprising gene trap cassette, and
PT   mutational element cassette that is transcriptionally silent, but which
PT   is activated by recombinase expression to disrupt expression of trapped
PT   gene.
XX
PS   Example 2; Page 35; 58pp; English.
XX
CC   The present invention provides recombinant vectors and methods of using
CC   the vectors in a high-throughput genetic system to rapidly generate
CC   conditional and/or conventional knockout mutants, e.g. in mice, useful
CC   for identifying and defining mammalian gene function in vivo. The methods
CC   combine gene trapping, gene targetting, and site-specific recombination
CC   techniques. The vectors comprise a transcriptionally silent mutational
CC   element that is inserted within a gene in a target cell in a manner that
CC   retains gene function, and which can be manipulated to inactivate the
CC   gene when desired. The mutational element may be flanked by mutant LoxP
CC   sites in a manner that produces a directional bias toward inversion of
CC   the mutational sequence upon exposure to cre recombinase. Once inverted,
CC   the mutational element is spliced into the trapped gene resulting in
CC   expression of a reporter gene and premature termination of the endogenous
CC   mRNA. Site-directed DNA integration is achieved using a pair of mutant
CC   loxP sites, a right element (RE) mutant (see ABN84176) and a left element
CC   (LE) mutant (present sequence). The mutant loxP system produces a
CC   reaction biased toward an irreversible gene inversion. The method of the
CC   invention facilitates investigation of the function of individual genes
CC   by a rapid extension of the conditional knockout approach
XX
SQ   Sequence 34 BP; 12 A; 5 C; 6 G; 11 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 3
ABA03775
ID   ABA03775 standard; DNA; 34 BP.
XX
AC   ABA03775;
XX
DT   19-FEB-2002  (first entry)
XX
DE   Synthetic lox71 sequence.
XX
KW   lox71; gene therapy; gene targeting; gene trapping;
KW   antisense RNA production; ds.
XX
OS   Synthetic.
XX
PN   WO200185973-A1.
XX
PD   15-NOV-2001.
XX
PF   29-AUG-2000; 2000WO-JP005824.
XX
PR   11-MAY-2000; 2000JP-00138938.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Taniguchi M,  Karasawa M;
XX
DR   WPI; 2002-055602/07.
XX
PT   Antisense type gene trap vector, useful for gene therapy of diseases and
PT   production of animal models for disease study, disrupts transcription of
PT   specific gene.
XX
PS   Claim 19; Page 42; 48pp; Japanese.
XX
CC   The invention relates to a method for producing cells in which the
CC   expression of a gene is disrupted. The cells are transformed with a gene
CC   trap vector to give a trap clone having the vector inserted at a specific
CC   mutation site of the target gene. The trap clone is then transformed with
CC   a vector that inserts a promoter in the antisense direction of the gene,
CC   enforcing transcription of antisense RNA. The method is useful for the
CC   production of animal models for studying human diseases. It is also
CC   useful as gene therapy for the treatment and prevention of diseases. The
CC   present sequence is a lox71 sequence claimed in the specification
XX
SQ   Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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```

```
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 4
ABZ20929
ID   ABZ20929 standard; DNA; 34 BP.
XX
AC   ABZ20929;
XX
DT   10-APR-2003  (first entry)
XX
DE   LoxP mutant with flanking sequence oligonucleotide #6.
XX
KW   Non-identical recognition sequence mutant; sequence-specific recombinase;
KW   recombination; antibiotic-resistance marker; loxP; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   DE10140030-C1.
XX
PD   19-DEC-2002.
XX
PF   16-AUG-2001; 2001DE-01040030.
XX
PR   16-AUG-2001; 2001DE-01040030.
XX
PA   (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI   Altmann M,  Neuhierl B,  Hammerschmidt W;
XX
DR   WPI; 2003-048025/05.
XX
PT   Method for performing multiple recombination events in a genetic system,
PT   useful e.g. for removing antibiotic resistance genes, uses mutant
PT   recombinase recognition sites.
XX
PS   Claim 3; Col 9; 10pp; German.
XX
CC   The present invention relates to the use of two non-identical recognition
CC   sequence mutants for a sequence-specific recombinase for performing two
CC   or more recombination events, mediated by the sequence-specific
CC   recombinase, in a single genetic system. The method is used to manipulate
CC   genetic systems (microbial, plant or animal) by site-specific
CC   recombination, e.g. to insert or remove DNA and most particularly to
CC   remove antibiotic-resistance markers. The present sequence was used to
CC   isolate the loxP coding sequence in the exemplification of the invention
XX
SQ   Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 8;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 5
ABZ20931
ID   ABZ20931 standard; DNA; 34 BP.
XX
AC   ABZ20931;
XX
DT   10-APR-2003  (first entry)
XX
DE   LoxP mutant with flanking sequence oligonucleotide #8.
XX
KW   Non-identical recognition sequence mutant; sequence-specific recombinase;
KW   recombination; antibiotic-resistance marker; loxP; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   DE10140030-C1.
XX
PD   19-DEC-2002.
XX
PF   16-AUG-2001; 2001DE-01040030.
XX
PR   16-AUG-2001; 2001DE-01040030.
XX
PA   (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI   Altmann M,  Neuhierl B,  Hammerschmidt W;
XX
DR   WPI; 2003-048025/05.
XX
PT   Method for performing multiple recombination events in a genetic system,
PT   useful e.g. for removing antibiotic resistance genes, uses mutant
PT   recombinase recognition sites.
XX
PS   Claim 4; Col 9; 10pp; German.
XX
CC   The present invention relates to the use of two non-identical recognition
CC   sequence mutants for a sequence-specific recombinase for performing two
CC   or more recombination events, mediated by the sequence-specific
CC   recombinase, in a single genetic system. The method is used to manipulate
CC   genetic systems (microbial, plant or animal) by site-specific
CC   recombination, e.g. to insert or remove DNA and most particularly to
CC   remove antibiotic-resistance markers. The present sequence was used to
CC   isolate the loxP coding sequence in the exemplification of the invention
XX
SQ   Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 8;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 6
ABZ79444
ID   ABZ79444 standard; DNA; 34 BP.
XX
AC   ABZ79444;
XX
DT   23-MAY-2003  (first entry)
XX
DE   Lox 71 DNA # SEQ ID 1.
XX
KW   LoxP; lox 71; knockout mouse; vascularisation; embryonic stem cell;
KW   drug development; locus of crossing over; ds.
XX
OS   Synthetic.
XX
PN   JP2002369689-A.
XX
PD   24-DEC-2002.
XX
PF   25-MAY-2001; 2001JP-00157568.
XX
PR   25-MAY-2001; 2001JP-00157568.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA   (IDEH/) IDE H.
PA   (YAMA/) YAMAMURA K.
PA   (ARAK/) ARAKI Y.
XX
DR   WPI; 2003-125824/12.
XX
PT   Knockout mouse or embryonic stem cells with introduced trap vectors
PT   containing a loxP sequence or a variant loxP sequence with disrupted gene
PT   of sequence No. 7 of 1405 bases.
```

```
XX
PS   Claim 4; Fig 4; 21pp; Japanese.
XX
CC   The invention relates to a knockout mouse or embryonic stem cells with
CC   introduced trap vectors containing a loxP sequence. The knockout animals
CC   of the invention may be used in the analysis of genomic functions,
CC   particularly for investigating the processes of vascularisation and the
CC   development of drugs participating in such processes. The current
CC   sequence represents lox 71
XX
SQ   Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 8;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 7
ACC85309
ID   ACC85309 standard; DNA; 34 BP.
XX
AC   ACC85309;
XX
DT   18-SEP-2003  (first entry)
XX
DE   Recombinase lox71 DNA recognition sequence.
XX
KW   Vegetable plastid transformation; transgenic; recognition sequence;
KW   plant; site-specific integration; nutrition; seed production;
KW   chemical production; ds.
XX
OS   Unidentified.
XX
PN   WO2003054201-A1.
XX
PD   03-JUL-2003.
XX
PF   16-DEC-2002; 2002WO-EP014303.
XX
PR   20-DEC-2001; 2001DE-01063159.
XX
PA   (SUNG-) SUNGENE GMBH & CO KGAA.
XX
PI   Biesgen C;
XX
DR   WPI; 2003-541820/51.
XX
PT   Site-specific integration of DNA into plastid DNA, useful for making
PT   transgenic plants used e.g. as food, by recombinase-mediated insertion.
XX
PS   Disclosure; Page 35; 164pp; German.
XX
CC   The present invention relates to a method for the site-specific
CC   integration of a DNA sequence into the plastid DNA of a plant or its
CC   derived cells. Transgenic plants in which a DNA sequence has been
CC   integrated, also their cell cultures, organs, tissues etc. are useful in
CC   human or animal nutrition, to produce seeds, and to produce
CC   pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,
CC   flavourings and aromatizing agents, dyes, antibodies and vaccines. The
CC   present sequence is a recognition sequence shown in the exemplification
CC   of the invention
XX
SQ   Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 9;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 8
ADD13802/c
ID   ADD13802 standard; DNA; 34 BP.
XX
AC   ADD13802;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Oligonucleotide lox71 DNA.
XX
KW   library; transfection; humanized monoclonal antibody; antigen;
KW   T cell receptor; primer; ss.
XX
OS   Synthetic.
XX
PN   EP1298207-A1.
XX
PD   02-APR-2003.
XX
PF   01-OCT-2001; 2001EP-00123596.
XX
PR   01-OCT-2001; 2001EP-00123596.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Breitling F,  Moldenhauer G,  Poustka A,  Kuehlwein T;
XX
DR   WPI; 2003-383833/37.
XX
PT   Preparing library of protein-producing eukaryotic cells, useful for
PT   producing humanized high-affinity antibodies, comprises introducing
PT   specific recombination signals into chromosomal gene loci and integrating
PT   a variety of DNA sequences.
XX
PS   Example 7; Page 15; 75pp; German.
XX
CC   This invention describes a novel method of preparing a library of protein
CC   -producing eukaryotic cells comprising (a) introducing specific
CC   recombination signals into one or two chromosomal gene loci, (b)
CC   Expanding at least one of the modified cells, (c) Transfecting many
CC   different DNA sequences, each flanked by recombination signals, into the
CC   expanded cells and (d) Integrating the DNA sequences into the gene loci
CC   on the basis of the recombination signals and the appropriate
CC   recombinase. The resulting cells express different proteins, each from an
CC   integrated DNA sequence and the proteins are bound to the cell surface.
CC   The method is particularly used to produce libraries of humanized
CC   monoclonal antibodies, for selection of those with affinity for
CC   particular antigens and useful for diagnostic or therapeutic use.
CC   Libraries of T cell receptors may also be prepared. The method produces
CC   libraries of high diversity; provides easy, quick and automatable
CC   selection from a large number of proteins, allows relatively simple
CC   alteration of the expressed gene (e.g. fusion to other protein-coding
CC   sequences), is suitable for large scale protein production and allows
CC   simple verification and characterization of selected cell lines. The
CC   method does not require incorporation of a resistance marker. This
CC   sequence represents oligonucleotide lox71.
XX
SQ   Sequence 34 BP; 12 A; 5 C; 6 G; 11 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 10;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 9
```

```
ADD15151
ID   ADD15151 standard; DNA; 34 BP.
XX
AC   ADD15151;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Variant loxP DNA recombination site designated lox71 (SeqID 3).
XX
KW   loxP site; circular; transgenic; plant; non-replicating; transgene;
KW   growth regulant; insect resistance; fungal disease resistance;
KW   stress resistance; ss; lox71.
XX
OS   Unidentified.
XX
PN   US2003100077-A1.
XX
PD   29-MAY-2003.
XX
PF   20-SEP-2001; 2001US-00957660.
XX
PR   20-SEP-2001; 2001US-00957660.
XX
PA   (KORT/) KORTE J A.
PA   (LOWE/) LOWE B A.
XX
PI   Korte JA,  Lowe BA;
XX
DR   WPI; 2003-777313/73.
XX
PT   Preparing a non-replicating, circular nucleic acid molecule useful for
PT   transforming crop plants to add desirable trait such as herbicide
PT   resistance, by amplifying starting circular nucleic acid molecule.
XX
PS   Claim 11; SEQ ID NO 3; 66pp; English.
XX
CC   This invention relates to an in vitro method to create circular molecules
CC   for use in transformation for the generation of transgenic plants.
CC   Specifically, it refers to a preparing a non-replicating, circular
CC   nucleic acid molecule using a first non-mutagenizing oligonucleotide
CC   primer with a nucleic acid sequence complementary to a selected sequence
CC   of the starting circular DNA molecule. As such, the present invention
CC   describes a method useful for preparing a fertile transgenic plant
CC   derived from a dicotyledonous plant preferably soybean and the transgenic
CC   cell is from a monocotyledon, preferably maize. The transgene can be a
CC   plant growth regulant with a selectable phenotype that confers an
CC   advantageous trait, for example, insect resistance, bacterial or fungal
CC   disease resistance, enhanced nutrient utilisation or stress resistance.
CC   This oligonucleotide sequence is a variant of the wild type loxP DNA
CC   recombination site known as lox71, used in an exemplification of the
CC   invention.
XX
SQ   Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 10;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 10
ABZ75319
ID   ABZ75319 standard; DNA; 34 BP.
XX
AC   ABZ75319;
XX
DT   29-APR-2003  (first entry)
XX
DE   Lox71 related sequence.
XX
KW   Lox71; knockout animal; Tubedown-1; genomic function analysis;
KW   organ development; ds.
XX
OS   Unidentified.
XX
PN   JP2002345477-A.
XX
PD   03-DEC-2002.
XX
PF   25-MAY-2001; 2001JP-00157567.
XX
PR   25-MAY-2001; 2001JP-00157567.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA   (IDEH/) IDE H.
PA   (YAMA/) YAMAMURA K.
PA   (ARAK/) ARAKI Y.
XX
DR   WPI; 2003-072475/07.
XX
PT   Knockout animals with introduced a trap vector containing a variant loxP
PT   with introduced variation in a part of sequence(s) of a spacer sequence,
PT   and reverse repetitive sequence 1 and/or 2.
XX
PS   Claim 3; Page 12; 22pp; Japanese.
XX
CC   The invention relates to novel knockout animals with the disrupted
CC   Tubedown-1 gene. The transgenic animals of the invention are useful for
CC   analysis of genomic functions, and establishment of an analytic system
CC   for the development of organs. The present sequence is related to Lox71
XX
SQ   Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 10;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 11
ABZ20936
ID   ABZ20936 standard; DNA; 44 BP.
XX
AC   ABZ20936;
XX
DT   10-APR-2003  (first entry)
XX
DE   Lox71 isolation oligonucleotide.
XX
KW   Non-identical recognition sequence mutant; sequence-specific recombinase;
KW   recombination; antibiotic-resistance marker; lox66; lox71; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   DE10140030-C1.
XX
PD   19-DEC-2002.
XX
PF   16-AUG-2001; 2001DE-01040030.
XX
PR   16-AUG-2001; 2001DE-01040030.
XX
PA   (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI   Altmann M,  Neuhierl B,  Hammerschmidt W;
XX
DR   WPI; 2003-048025/05.
XX
PT   Method for performing multiple recombination events in a genetic system,
```

```
PT   useful e.g. for removing antibiotic resistance genes, uses mutant
PT   recombinase recognition sites.
XX
PS   Example; Fig 1; 10pp; German.
XX
CC   The present invention relates to the use of two non-identical recognition
CC   sequence mutants for a sequence-specific recombinase for performing two
CC   or more recombination events, mediated by the sequence-specific
CC   recombinase, in a single genetic system. The method is used to manipulate
CC   genetic systems (microbial, plant or animal) by site-specific
CC   recombination, e.g. to insert or remove DNA and most particularly to
CC   remove antibiotic-resistance markers. The present sequence was used to
CC   isolate the lox66 and lox71 coding sequences in the exemplification of
CC   the invention
XX
SQ   Sequence 44 BP; 11 A; 10 C; 6 G; 17 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 8;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39


RESULT 12
ABZ20922
ID   ABZ20922 standard; DNA; 68 BP.
XX
AC   ABZ20922;
XX
DT   10-APR-2003  (first entry)
XX
DE   Lox66 and lox71 isolation oligonucleotide #1.
XX
KW   Non-identical recognition sequence mutant; sequence-specific recombinase;
KW   recombination; antibiotic-resistance marker; lox66; lox71; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   DE10140030-C1.
XX
PD   19-DEC-2002.
XX
PF   16-AUG-2001; 2001DE-01040030.
XX
PR   16-AUG-2001; 2001DE-01040030.
XX
PA   (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI   Altmann M,  Neuhierl B,  Hammerschmidt W;
XX
DR   WPI; 2003-048025/05.
XX
PT   Method for performing multiple recombination events in a genetic system,
PT   useful e.g. for removing antibiotic resistance genes, uses mutant
PT   recombinase recognition sites.
XX
PS   Example; Col 6; 10pp; German.
XX
CC   The present invention relates to the use of two non-identical recognition
CC   sequence mutants for a sequence-specific recombinase for performing two
CC   or more recombination events, mediated by the sequence-specific
CC   recombinase, in a single genetic system. The method is used to manipulate
CC   genetic systems (microbial, plant or animal) by site-specific
CC   recombination, e.g. to insert or remove DNA and most particularly to
CC   remove antibiotic-resistance markers. The present sequence was used to
CC   isolate the lox66 and lox71 coding sequences in the exemplification of
CC   the invention
XX
SQ   Sequence 68 BP; 16 A; 16 C; 14 G; 22 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 8;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 0.0002;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         11 TACCGTTCGTATAGCATACATTATACGAAGTTAT 44


RESULT 13
AAD04925/c
ID   AAD04925 standard; DNA; 78 BP.
XX
AC   AAD04925;
XX
DT   17-JUL-2001  (first entry)
XX
DE   Primer lox3 for synthesising DNA fragment with loxP mutant sites.
XX
KW   Gene trapping construct; conditional mutation; unidirectional inversion;
KW   recombinase recognition sequence; RRS; disruption cassette;
KW   selection cassette; transgenic organism; loxP site; primer; ss.
XX
OS   Enterobacteria phage P1.
OS   Synthetic.
XX
PN   WO200129208-A1.
XX
PD   26-APR-2001.
XX
PF   16-OCT-2000; 2000WO-EP010162.
XX
PR   16-OCT-1999;   99EP-00120592.
PR   27-OCT-1999;   99US-0162016P.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
PA   (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI   Kuehn R,  Von Melchener H,  Altschmied J;
XX
DR   WPI; 2001-308486/32.
XX
PT   New gene trapping construct capable of causing conditional mutations in
PT   genes, comprises functional DNA segment inserted in sense or antisense
PT   direction relative to gene to be trapped.
XX
PS   Example 1; Page 18; 78pp; English.
XX
CC   The present invention relates to a conditional gene trapping construct
CC   capable of causing conditional mutations in genes. The gene trapping
CC   construct comprises two functional DNA segments, each being flanked by
CC   two recombinase recognition sequences (RRSs) specific to site specific
CC   recombinase which is capable of unidirectional inversion of double
CC   standard DNA segment. One of the DNA segment (disruption cassette) is
CC   inserted in antisense orientation relative to the transcriptional
CC   orientation of the gene to be trapped. The other DNA segment (selection
CC   cassette) is inserted in sense direction relative to the transcriptional
CC   orientation of the gene to be trapped. The cell comprising the gene
CC   trapping construct is useful for the identification and/or isolation of
CC   genes. The transgenic organism comprising the gene trapping construct is
CC   useful to study gene function at various developmental stages. The gene
CC   trapping construct is useful for mutationally inactivating all cellular
CC   genes. The present sequence is a primer lox3 which is used for
CC   synthesising a DNA fragment containing a lox66 and a lox71 Cre
CC   recombinase recognition mutant sites in opposite orientation. The primer
CC   is used for constructing the gene trap vector pRK57SA-beta
XX
SQ   Sequence 78 BP; 27 A; 14 C; 14 G; 23 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 34;  DB 5;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 0.00021;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         78 TACCGTTCGTATAGCATACATTATACGAAGTTAT 45
```

```
RESULT 14
AAD04926
ID   AAD04926 standard; DNA; 79 BP.
XX
AC   AAD04926;
XX
DT   17-JUL-2001  (first entry)
XX
DE   Primer lox4 for synthesising DNA fragment with loxP mutant sites.
XX
KW   Gene trapping construct; conditional mutation; unidirectional inversion;
KW   recombinase recognition sequence; RRS; disruption cassette;
KW   selection cassette; transgenic organism; loxP site; primer; ss.
XX
OS   Enterobacteria phage P1.
OS   Synthetic.
XX
PN   WO200129208-A1.
XX
PD   26-APR-2001.
XX
PF   16-OCT-2000; 2000WO-EP010162.
XX
PR   16-OCT-1999;   99EP-00120592.
PR   27-OCT-1999;   99US-0162016P.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
PA   (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI   Kuehn R,  Von Melchener H,  Altschmied J;
XX
DR   WPI; 2001-308486/32.
XX
PT   New gene trapping construct capable of causing conditional mutations in
PT   genes, comprises functional DNA segment inserted in sense or antisense
PT   direction relative to gene to be trapped.
XX
PS   Example 1; Page 18-19; 78pp; English.
XX
CC   The present invention relates to a conditional gene trapping construct
CC   capable of causing conditional mutations in genes. The gene trapping
CC   construct comprises two functional DNA segments, each being flanked by
CC   two recombinase recognition sequences (RRSs) specific to site specific
CC   recombinase which is capable of unidirectional inversion of double
CC   standard DNA segment. One of the DNA segment (disruption cassette) is
CC   inserted in antisense orientation relative to the transcriptional
CC   orientation of the gene to be trapped. The other DNA segment (selection
CC   cassette) is inserted in sense direction relative to the transcriptional
CC   orientation of the gene to be trapped. The cell comprising the gene
CC   trapping construct is useful for the identification and/or isolation of
CC   genes. The transgenic organism comprising the gene trapping construct is
CC   useful to study gene function at various developmental stages. The gene
CC   trapping construct is useful for mutationally inactivating all cellular
CC   genes. The present sequence is a primer lox4 which is used for
CC   synthesising a DNA fragment containing a lox66 and a lox71 Cre
CC   recombinase recognition mutant sites in opposite orientation. The primer
CC   is used for constructing the gene trap vector pRK57SA-beta
XX
SQ   Sequence 79 BP; 24 A; 14 C; 14 G; 27 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 5;  Length 79;
  Best Local Similarity  100.0%;  Pred. No. 0.00021;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39
```

```
RESULT 15
ABV75994
ID   ABV75994 standard; DNA; 94 BP.
XX
AC   ABV75994;
XX
DT   11-FEB-2003  (first entry)
XX
DE   OLIGO-F, contains attP and attB sites for phage phi-C31 integrase.
XX
KW   AttP; attB; phage phi-C31; integrase; recombination; minicircle;
KW   gene therapy; mitochondria; ss.
XX
OS   Bacteriophage phi-C31.
OS   Synthetic.
XX
PN   WO200283889-A2.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2002; 2002WO-GB001668.
XX
PR   10-APR-2001; 2001GB-00008968.
PR   05-OCT-2001; 2001US-0327029P.
XX
PA   (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI   Bigger BW,  Tolmachov O,  Coutelle C;
XX
DR   WPI; 2003-075546/07.
XX
PT   New cell capable of expressing an endonuclease, useful for producing a
PT   minicircle for mitochondrial gene therapy, comprises a parent plasmid
PT   capable of recombination to form a minicircle and a miniplasmid.
XX
PS   Example 3; Page 46; 70pp; English.
XX
CC   The present sequence is that of oligonucleotide OLIGO-F, which was
CC   annealed to OLIGO-R (see ABV75995) and introduced into plasmid pBC-SK(+),
CC   thereby creating attP and attB recombination sites. Minicircle-producing
CC   plasmids with attP and attB sites for phage phi-C31 integrase were
CC   constructed. This is an example of a method of the invention for the
CC   production of a minicircle. In this method, a plasmid having a DNA
CC   sequence flanked by attP and attB sites is exposed to phi-C31 integrase,
CC   thereby forming a minicircle comprising the DNA sequence and a
CC   miniplasmid comprising the remainder of the plasmid. The minicircle is
CC   useful for mitochondrial gene therapy
XX
SQ   Sequence 94 BP; 33 A; 19 C; 15 G; 27 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 8;  Length 94;
  Best Local Similarity  100.0%;  Pred. No. 0.00021;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db         50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83


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GenCore version 5.1.6

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	1	29	85.3	34	1	US-08-214-023-1	Sequence 1, Appli
	2	29	85.3	34	1	US-08-214-023-2	Sequence 2, Appli
	3	29	85.3	34	1	US-08-615-048-1	Sequence 1, Appli
	4	29	85.3	34	2	US-08-864-224-12	Sequence 12, Appl
c	5	29	85.3	34	2	US-08-743-796-1	Sequence 1, Appli
c	6	29	85.3	34	2	US-08-350-260A-1	Sequence 1, Appli
c	7	29	85.3	34	2	US-08-350-260A-601	Sequence 601, App
c	8	29	85.3	34	3	US-08-654-623-4	Sequence 4, Appli
c	9	29	85.3	34	3	US-09-011-257-1	Sequence 1, Appli
c	10	29	85.3	34	3	US-08-412-777-1	Sequence 1, Appli
c	11	29	85.3	34	3	US-08-412-826-1	Sequence 1, Appli
	12	29	85.3	34	3	US-09-214-471-1	Sequence 1, Appli
	13	29	85.3	34	3	US-09-193-475-1	Sequence 1, Appli
c	14	29	85.3	34	3	US-09-563-239-1	Sequence 1, Appli
c	15	29	85.3	34	3	US-09-271-055A-1	Sequence 1, Appli
c	16	29	85.3	34	3	US-09-603-663-1	Sequence 1, Appli
	17	29	85.3	34	3	US-09-603-663-5	Sequence 5, Appli
c	18	29	85.3	34	3	US-09-603-658-1	Sequence 1, Appli
	19	29	85.3	34	3	US-09-603-658-5	Sequence 5, Appli
c	20	29	85.3	34	3	US-09-602-373A-1	Sequence 1, Appli
	21	29	85.3	34	3	US-09-602-373A-5	Sequence 5, Appli
	22	29	85.3	34	3	US-09-661-364-1	Sequence 1, Appli
c	23	29	85.3	34	3	US-09-610-259-1	Sequence 1, Appli
c	24	29	85.3	34	3	US-09-554-271A-1	Sequence 1, Appli
c	25	29	85.3	34	3	US-09-837-863-1	Sequence 1, Appli
c	26	29	85.3	34	4	US-09-104-337A-1	Sequence 1, Appli
c	27	29	85.3	34	4	US-09-293-303-1	Sequence 1, Appli
c	28	29	85.3	34	4	US-09-718-034-2	Sequence 2, Appli
c	29	29	85.3	34	4	US-09-606-323C-1	Sequence 1, Appli
c	30	29	85.3	34	4	US-09-703-399A-1	Sequence 1, Appli
	31	29	85.3	34	4	US-09-703-399A-5	Sequence 5, Appli
	32	29	85.3	34	4	US-09-377-885A-1	Sequence 1, Appli
c	33	29	85.3	34	4	US-09-377-885A-20	Sequence 20, Appl
	34	29	85.3	34	4	US-09-975-304-1	Sequence 1, Appli
	35	29	85.3	34	4	US-09-411-826-1	Sequence 1, Appli
c	36	29	85.3	34	4	US-10-072-047-1	Sequence 1, Appli
	37	29	85.3	34	4	US-09-662-128A-3	Sequence 3, Appli
c	38	29	85.3	34	4	US-09-856-110B-1	Sequence 1, Appli
	39	29	85.3	34	4	US-09-856-110B-2	Sequence 2, Appli
	40	29	85.3	34	4	US-09-937-837-5	Sequence 5, Appli
c	41	29	85.3	34	4	US-09-829-507-1	Sequence 1, Appli
	42	29	85.3	34	4	US-09-122-384-12	Sequence 12, Appl
	43	29	85.3	34	4	US-09-329-582A-1	Sequence 1, Appli
c	44	29	85.3	34	5	PCT-US93-00108-1	Sequence 1, Appli
	45	29	85.3	34	5	PCT-US93-00108-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-08-214-023-1/c
; Sequence 1, Application US/08214023
; Patent No. 5434066
;  GENERAL INFORMATION:
;    APPLICANT:  BEBEE, ROBERT L
;    APPLICANT:  HARTLEY, JAMES L
;    TITLE OF INVENTION:  MODULATION OF ENZYME ACTIVITIES IN THE
;    TITLE OF INVENTION:  IN VIVO CLONING OF DNA
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WEIL, GOTSHAL & MANGES
;      STREET:  1615 L STREET, N.W.; SUITE 700
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/214,023
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/862,188
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I
;      REGISTRATION NUMBER:  32,680
;      REFERENCE/DOCKET NUMBER:  59452.0011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 682-7033
;      TELEFAX:  (202) 859-0939
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  ESCHERICHIA COLI
;      STRAIN:  DH1OB
US-08-214-023-1
```

```
  Query Match             85.3%;  Score 29;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 2
US-08-214-023-2
; Sequence 2, Application US/08214023
; Patent No. 5434066
;  GENERAL INFORMATION:
;    APPLICANT:  BEBEE, ROBERT L
;    APPLICANT:  HARTLEY, JAMES L
;    TITLE OF INVENTION:  MODULATION OF ENZYME ACTIVITIES IN THE
;    TITLE OF INVENTION:  IN VIVO CLONING OF DNA
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WEIL, GOTSHAL & MANGES
;      STREET:  1615 L STREET, N.W.; SUITE 700
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/214,023
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/862,188
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I
;      REGISTRATION NUMBER:  32,680
;      REFERENCE/DOCKET NUMBER:  59452.0011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 682-7033
;      TELEFAX:  (202) 859-0939
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  ESCHERICHIA COLI
;      STRAIN:  DH1OB
US-08-214-023-2

  Query Match             85.3%;  Score 29;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db          6 TTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 3
US-08-615-048-1
; Sequence 1, Application US/08615048
; Patent No. 5700470
;  GENERAL INFORMATION:
;    APPLICANT:  Saito, Izumu
;    APPLICANT:  Kanegae, Yumi
;    APPLICANT:  Nakai, Michio
;    TITLE OF INVENTION:  RECOMBINANT DNA VIRUS AND METHOD FOR
;    TITLE OF INVENTION:  PREPARATION THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/615,048
;      FILING DATE:  12-MAR-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nakamura, Dean H.
;      REGISTRATION NUMBER:  33,981
;      REFERENCE/DOCKET NUMBER:  Q-41057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-615-048-1

  Query Match             85.3%;  Score 29;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db          6 TTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 4
US-08-864-224-12
; Sequence 12, Application US/08864224
; Patent No. 5851808
;  GENERAL INFORMATION:
;    APPLICANT:  Elledge, Stephen J.
;    APPLICANT:  Liu, Qinghua
;    TITLE OF INVENTION:  Rapid Subcloning Using Site-Specific
;    TITLE OF INVENTION:  Recombination
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,224
;      FILING DATE:
;      CLASSIFICATION:  435
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  BCM-02681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "DNA"
US-08-864-224-12

  Query Match             85.3%;  Score 29;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db          6 TTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 5
US-08-743-796-1/c
; Sequence 1, Application US/08743796
; Patent No. 5928914
;  GENERAL INFORMATION:
;    APPLICANT:  Leboulch, P. et al.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TRANSFORMING CELLS
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/743,796
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane E. Remillard
;      REGISTRATION NUMBER:  38,872
;      REFERENCE/DOCKET NUMBER:  MTE-198
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-743-796-1

  Query Match             85.3%;  Score 29;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 6
US-08-350-260A-1/c
; Sequence 1, Application US/08350260A
; Patent No. 5962255
;  GENERAL INFORMATION:
;    APPLICANT:  Winter, Gregory Paul
;    APPLICANT:  Griffiths, Andrew David
;    APPLICANT:  Williams, Samuel Cameron
;    APPLICANT:  Waterhouse, Peter
;    APPLICANT:  Nissim, Ahuva
;    APPLICANT:  Johnson, Kevin Stuart
;    APPLICANT:  Smith, Andrew John Hammond
;    TITLE OF INVENTION:  Methods for producing members of specific
;    TITLE OF INVENTION:  binding pairs
;    NUMBER OF SEQUENCES:  602
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough
;      STREET:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/350,260A
;      FILING DATE:  05-DEC-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9110549.4
;      FILING DATE:  15-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB91/01134
;      FILING DATE:  10-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/00605
;      FILING DATE:  24-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/150,002
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/307,619
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/32372
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
US-08-350-260A-1
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  Query Match             85.3%;  Score 29;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 7
US-08-350-260A-601/c
; Sequence 601, Application US/08350260A
; Patent No. 5962255
;  GENERAL INFORMATION:
;    APPLICANT:  Winter, Gregory Paul
;    APPLICANT:  Griffiths, Andrew David
;    APPLICANT:  Williams, Samuel Cameron
;    APPLICANT:  Waterhouse, Peter
;    APPLICANT:  Nissim, Ahuva
;    APPLICANT:  Johnson, Kevin Stuart
;    APPLICANT:  Smith, Andrew John Hammond
;    TITLE OF INVENTION:  Methods for producing members of specific
;    TITLE OF INVENTION:  binding pairs
;    NUMBER OF SEQUENCES:  602
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough
;      STREET:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/350,260A
;      FILING DATE:  05-DEC-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9110549.4
;      FILING DATE:  15-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB91/01134
;      FILING DATE:  10-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/00605
;      FILING DATE:  24-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/150,002
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/307,619
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/32372
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  601:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-350-260A-601

  Query Match             85.3%;  Score 29;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 8
US-08-654-623-4/c
; Sequence 4, Application US/08654623
; Patent No. 6010884
;  GENERAL INFORMATION:
;    APPLICANT:  Griffiths, Andrew D
;    APPLICANT:  Holliger, Kaspar-Philipp
;    APPLICANT:  Nissim, Ahuva
;    APPLICANT:  Fisch, Igor
;    APPLICANT:  Winter, Gregory P
;    TITLE OF INVENTION:  Recombinant Binding Proteins and Peptides
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/654,623
;      FILING DATE:  29-MAY-1996
;      CLASSIFICATION:  435
;      CLASSIFICATION:  (C12N 1/21, C12R 1:19)
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9225453.1
;      FILING DATE:  04-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9300816.7
;      FILING DATE:  16-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93303614.7
;      FILING DATE:  10-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9319969.3
;      FILING DATE:  22-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/02492
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9412147.2
;      FILING DATE:  17-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/02662
;      FILING DATE:  05-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/448,418
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33259
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;  INFORMATION FOR SEQ ID NO:  4:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  Other nucleic acid: plasmid DNA
US-08-654-623-4

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 9
US-09-011-257-1/c
; Sequence 1, Application US/09011257
; Patent No. 6066478
; GENERAL INFORMATION:
;  APPLICANT: LUSKY, Monika
;  APPLICANT: MEHTALI, Majid
;  TITLE OF INVENTION: HELPER VIRUSES FOR PREPARING RECOMBINANT VIRAL VECTORS
;  FILE REFERENCE: 017753-090
;  CURRENT APPLICATION NUMBER: US/09/011,257
;  CURRENT FILING DATE: 1998-03-09
;  EARLIER APPLICATION NUMBER: FR 95/09.289
;  EARLIER FILING DATE: 1995-07-31
;  EARLIER APPLICATION NUMBER: PCT/FR96/01200
;  EARLIER FILING DATE: 1996-07-30
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Bacteriophage P1
US-09-011-257-1

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 10
US-08-412-777-1/c
; Sequence 1, Application US/08412777
; Patent No. 6091001
;  GENERAL INFORMATION:
;    APPLICANT:  JAKOBOVITS, AYA
;    APPLICANT:  ZSEBO, KRISZTINA M.
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES USING
;    TITLE OF INVENTION:  CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CELL GENESYS, INC.
;      STREET:  322 LAKESIDE DRIVE
;      CITY:  FOSTER CITY
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/412,777
;      FILING DATE:  29-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDEL, SARALYNN
;      REGISTRATION NUMBER:  31,853
;      REFERENCE/DOCKET NUMBER:  CELL20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)358-9600 X345
;      TELEFAX:  (415)349-7392
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-412-777-1

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 11
US-08-412-826-1/c
; Sequence 1, Application US/08412826
; Patent No. 6130364
;  GENERAL INFORMATION:
;    APPLICANT:  JAKOBOVITS, AYA
;    APPLICANT:  ZSEBO, KRISZTINA M.
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES USING
;    TITLE OF INVENTION:  CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CELL GENESYS, INC.
;      STREET:  322 LAKESIDE DRIVE
;      CITY:  FOSTER CITY
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/412,826
;      FILING DATE:  29-MAR-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDEL, SARALYNN
;      REGISTRATION NUMBER:  31,853
;      REFERENCE/DOCKET NUMBER:  CELL21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)358-9600 X345
;      TELEFAX:  (415)349-7392
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-412-826-1

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
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  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
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Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 12
US-09-214-471-1
; Sequence 1, Application US/09214471
; Patent No. 6201166
; GENERAL INFORMATION:
;  APPLICANT: Kohara, Michinori
;  APPLICANT: Wakita, Takaji
;  APPLICANT: Yonekawa, Hiromichi
;  APPLICANT: Taya, Choji
;  APPLICANT: Saito, Izumu
;  TITLE OF INVENTION: Hepatitis C Animal Model
;  FILE REFERENCE: sequence listing 382.1025
;  CURRENT APPLICATION NUMBER: US/09/214,471
;  CURRENT FILING DATE: 1999-01-21
;  EARLIER APPLICATION NUMBER: PCT/JP97/02575
;  EARLIER FILING DATE: 1997-07-24
;  EARLIER APPLICATION NUMBER: 195076/1996 JAPAN
;  EARLIER FILING DATE: 1996-07-24
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: E. coli P1 phage
US-09-214-471-1

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
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Db          6 TTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 13
US-09-193-475-1
; Sequence 1, Application US/09193475
; Patent No. 6300545
; GENERAL INFORMATION:
;  APPLICANT: Baszczynski, Christopher L.
;  APPLICANT: Lyznik, Leszek
;  APPLICANT: Gordon-Kamm, William J.
;  APPLICANT: Guan, Xueni
;  TITLE OF INVENTION: Mobilization of Viral Genomes From T-DNA
;  TITLE OF INVENTION: Using Site-Specific Recombination Systems
;  FILE REFERENCE: 5718-61
;  CURRENT APPLICATION NUMBER: US/09/193,475
;  CURRENT FILING DATE: 1998-11-17
;  EARLIER APPLICATION NUMBER: 60/099,461
;  EARLIER FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: 60/065,627
;  EARLIER FILING DATE: 1997-11-18
;  EARLIER APPLICATION NUMBER: 60/065,613
;  EARLIER FILING DATE: 1997-11-18
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: wild type loxP recombination site
US-09-193-475-1

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
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Db          6 TTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 14
US-09-563-239-1/c
; Sequence 1, Application US/09563239
; Patent No. 6350575
; GENERAL INFORMATION:
;  APPLICANT: LUSKY, Monika
;  APPLICANT:  MEHTALI, Majid
;  TITLE OF INVENTION: HELPER VIRUSES FOR PREPARING RECOMBINANT VIRAL VECTORS
;  FILE REFERENCE: 017753-090
;  CURRENT APPLICATION NUMBER: US/09/563,239
;  CURRENT FILING DATE:  2000-05-02
;  PRIOR APPLICATION NUMBER: 09/011,257
;  PRIOR FILING DATE: 1998-03-09
;  PRIOR APPLICATION NUMBER: PCT/FR96/01200
;  PRIOR FILING DATE: 1996-07-30
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Bacteriophage P1
US-09-563-239-1

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  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 15
US-09-271-055A-1/c
; Sequence 1, Application US/09271055A
; Patent No. 6406847
; GENERAL INFORMATION:
;  APPLICANT: David Cox
;  APPLICANT:  Malek Fahan
;  APPLICANT:  Siamak Baharloo
;  TITLE OF INVENTION: Mismatch Repair Detection
;  FILE REFERENCE: UCSF-127CIP
;  CURRENT APPLICATION NUMBER: US/09/271,055A
;  CURRENT FILING DATE:  1999-03-17
;  PRIOR APPLICATION NUMBER: 08/713,751
;  PRIOR FILING DATE: 1996-09-13
;  PRIOR APPLICATION NUMBER: 60/004,664
;  PRIOR FILING DATE: 1995-10-02
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: lambda phage
US-09-271-055A-1

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTCGTATAGCATACATTATACGAAGTTAT 34
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Db         29 TTCGTATAGCATACATTATACGAAGTTAT 1


Search completed: September  8, 2005, 21:11:10
Job time : 71 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 20:55:38 ; Search time 309 Seconds
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Title: US-10-030-658B-15
Perfect score: 34
Sequence: 1 taccgttcgtatagcatacattatacgaagttat 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		34	100.0	34	10	US-09-957-660-3	Sequence 3, Appli
2		34	100.0	34	14	US-10-214-722-6	Sequence 6, Appli
3		34	100.0	34	14	US-10-214-722-8	Sequence 8, Appli
	c 4	34	100.0	34	18	US-10-416-995-9	Sequence 9, Appli
5		34	100.0	34	19	US-10-739-769-3	Sequence 3, Appli
	c 6	34	100.0	34	20	US-10-448-395-2	Sequence 2, Appli
	c 7	34	100.0	34	20	US-10-448-395-13	Sequence 13, Appl
8		34	100.0	40	20	US-10-448-395-15	Sequence 15, Appl
	c 9	34	100.0	40	20	US-10-448-395-16	Sequence 16, Appl
10		34	100.0	44	14	US-10-214-722-15	Sequence 15, Appl
11		34	100.0	68	14	US-10-214-722-11	Sequence 11, Appl
12		34	100.0	94	14	US-10-118-231-10	Sequence 10, Appl
13		34	100.0	94	14	US-10-118-231-16	Sequence 16, Appl
	c 14	34	100.0	2133	20	US-10-448-395-1	Sequence 1, Appli
15		32.4	95.3	34	14	US-10-214-722-7	Sequence 7, Appli
16		30.8	90.6	34	14	US-10-214-722-9	Sequence 9, Appli
	c 17	30.8	90.6	34	19	US-10-739-769-5	Sequence 5, Appli
18		29	85.3	32	10	US-09-999-321-1	Sequence 1, Appli
19		29	85.3	32	16	US-10-301-516-13	Sequence 13, Appl
	c 20	29	85.3	34	9	US-09-829-507-1	Sequence 1, Appli
	c 21	29	85.3	34	9	US-09-920-932-1	Sequence 1, Appli
	c 22	29	85.3	34	9	US-09-908-305-3	Sequence 3, Appli
23		29	85.3	34	9	US-09-908-305-4	Sequence 4, Appli
24		29	85.3	34	9	US-09-804-653-4	Sequence 4, Appli
25		29	85.3	34	9	US-09-822-634-3	Sequence 3, Appli
	c 26	29	85.3	34	9	US-09-945-952A-4	Sequence 4, Appli
	c 27	29	85.3	34	10	US-09-948-193-3	Sequence 3, Appli
28		29	85.3	34	10	US-09-377-885A-1	Sequence 1, Appli
	c 29	29	85.3	34	10	US-09-377-885A-20	Sequence 20, Appl
30		29	85.3	34	10	US-09-981-397A-6	Sequence 6, Appli
	c 31	29	85.3	34	10	US-09-997-209-29	Sequence 29, Appl
32		29	85.3	34	10	US-09-990-185-7	Sequence 7, Appli
33		29	85.3	34	10	US-09-957-660-1	Sequence 1, Appli
34		29	85.3	34	10	US-09-957-660-4	Sequence 4, Appli
35		29	85.3	34	10	US-09-975-304-1	Sequence 1, Appli
	c 36	29	85.3	34	10	US-09-843-150-52	Sequence 52, Appl
	c 37	29	85.3	34	10	US-09-843-150-53	Sequence 53, Appl
	c 38	29	85.3	34	13	US-10-072-047-1	Sequence 1, Appli
	c 39	29	85.3	34	13	US-10-057-050-2	Sequence 2, Appli
	c 40	29	85.3	34	14	US-10-081-771-1	Sequence 1, Appli
	c 41	29	85.3	34	14	US-10-029-471-3	Sequence 3, Appli
42		29	85.3	34	14	US-10-029-471-4	Sequence 4, Appli
	c 43	29	85.3	34	14	US-10-210-425-1	Sequence 1, Appli
	c 44	29	85.3	34	14	US-10-112-612-1	Sequence 1, Appli
45		29	85.3	34	14	US-10-112-612-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-957-660-3
; Sequence 3, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; APPLICANT: LOWE, BRENDA A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; TITLE OF INVENTION: TRANSFORMATION
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-957-660-3

Query Match 100.0%; Score 34; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

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RESULT 2
US-10-214-722-6
; Sequence 6, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
;  APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
;  TITLE OF INVENTION: The use of mutated recognition sequences for multiple
;  TITLE OF INVENTION:  consecutive recombinase-mediated recombinations
;  TITLE OF INVENTION:  in a genetic system
;  FILE REFERENCE: P14567
;  CURRENT APPLICATION NUMBER: US/10/214,722
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: DE 101 40 030.6
;  PRIOR FILING DATE: 2001-08-16
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence:
;   OTHER INFORMATION: Oligonucleotide lox 71 without flanks
US-10-214-722-6

  Query Match           100.0%;  Score 34;  DB 14;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.00057;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 3
US-10-214-722-8
; Sequence 8, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
;  APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
;  TITLE OF INVENTION: The use of mutated recognition sequences for multiple
;  TITLE OF INVENTION:  consecutive recombinase-mediated recombinations
;  TITLE OF INVENTION:  in a genetic system
;  FILE REFERENCE: P14567
;  CURRENT APPLICATION NUMBER: US/10/214,722
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: DE 101 40 030.6
;  PRIOR FILING DATE: 2001-08-16
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-214-722-8

  Query Match           100.0%;  Score 34;  DB 14;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.00057;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 4
US-10-416-995-9/c
; Sequence 9, Application US/10416995
; Publication No. US20040077089A1
; GENERAL INFORMATION:
;  APPLICANT: Xin, Hong-Bo
;  APPLICANT:  Kotlikoff, Michael
;  APPLICANT:  Cornell Research Foundation, Inc.
;  TITLE OF INVENTION: VECTORS FOR CONDITIONAL GENE INACTIVATION
;  FILE REFERENCE: 1153.020US1
;  CURRENT APPLICATION NUMBER: US/10/416,995
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: PCT/US01/43916
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: US 60/249,200
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A mutant loxP sequence
US-10-416-995-9

  Query Match           100.0%;  Score 34;  DB 18;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.00057;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 5
US-10-739-769-3
; Sequence 3, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
;  APPLICANT: Monsanto Technology, LLC
;  TITLE OF INVENTION: Methods of Site-Directed Transformation
;  FILE REFERENCE: 38-15(52823)B
;  CURRENT APPLICATION NUMBER: US/10/739,769
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: variant of wild-type loxP recombination site
US-10-739-769-3

  Query Match           100.0%;  Score 34;  DB 19;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.00057;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||||||
Db          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34


RESULT 6
US-10-448-395-2/c
; Sequence 2, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
;  APPLICANT: Askew, G. Roger
;  APPLICANT:  Kanki, Kim L
;  APPLICANT:  Barton, Michael
;  TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
;  TITLE OF INVENTION:  Using an Inducible Gene Silencer
;  FILE REFERENCE: 01997.026400
;  CURRENT APPLICATION NUMBER: US/10/448,395
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; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-2

Query Match 100.0%; Score 34; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db 34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 7
US-10-448-395-13/c
; Sequence 13, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; TITLE OF INVENTION: Using an Inducible Gene Silencer
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-13

Query Match 100.0%; Score 34; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db 34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 8
US-10-448-395-15
; Sequence 15, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; TITLE OF INVENTION: Using an Inducible Gene Silencer
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-448-395-15

Query Match 100.0%; Score 34; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db 6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39

RESULT 9
US-10-448-395-16/c
; Sequence 16, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; TITLE OF INVENTION: Using an Inducible Gene Silencer
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-448-395-16

Query Match 100.0%; Score 34; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
||||||||||||||||||||||||||||||||||
Db 39 TACCGTTCGTATAGCATACATTATACGAAGTTAT 6

RESULT 10
US-10-214-722-15
; Sequence 15, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombinase-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 71 with flanks
US-10-214-722-15

Query Match 100.0%; Score 34; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

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Db          6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39


RESULT 11
US-10-214-722-11
; Sequence 11, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
;  APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
;  TITLE OF INVENTION: The use of mutated recognition sequences for multiple
;  TITLE OF INVENTION:  consecutive recombinase-mediated recombinations
;  TITLE OF INVENTION:  in a genetic system
;  FILE REFERENCE: P14567
;  CURRENT APPLICATION NUMBER: US/10/214,722
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: DE 101 40 030.6
;  PRIOR FILING DATE: 2001-08-16
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 68
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-214-722-11

  Query Match             100.0%;  Score 34;  DB 14;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 0.00064;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
                ||||||||||||||||||||||||||||||||||
Db         11 TACCGTTCGTATAGCATACATTATACGAAGTTAT 44


RESULT 12
US-10-118-231-10
; Sequence 10, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
;  APPLICANT: Bigger, Brian W
;  APPLICANT:  Tolmachov, Oleg
;  APPLICANT:  Coutelle, Charles
;  TITLE OF INVENTION: Methods
;  FILE REFERENCE: 102286.141US
;  CURRENT APPLICATION NUMBER: US/10/118,231
;  CURRENT FILING DATE:  2002-04-09
;  PRIOR APPLICATION NUMBER: US 60/327,029
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: GB 0108968.9
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 94
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-118-231-10

  Query Match             100.0%;  Score 34;  DB 14;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 0.00067;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
                ||||||||||||||||||||||||||||||||||
Db         50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83


RESULT 13
US-10-118-231-16
; Sequence 16, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
;  APPLICANT: Bigger, Brian W
;  APPLICANT:  Tolmachov, Oleg
;  APPLICANT:  Coutelle, Charles
;  TITLE OF INVENTION: Methods
;  FILE REFERENCE: 102286.141US
;  CURRENT APPLICATION NUMBER: US/10/118,231
;  CURRENT FILING DATE:  2002-04-09
;  PRIOR APPLICATION NUMBER: US 60/327,029
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: GB 0108968.9
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 94
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-118-231-16

  Query Match             100.0%;  Score 34;  DB 14;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 0.00067;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
                ||||||||||||||||||||||||||||||||||
Db         50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83


RESULT 14
US-10-448-395-1/c
; Sequence 1, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
;  APPLICANT: Askew, G. Roger
;  APPLICANT:  Kanki, Kim  L
;  APPLICANT:  Barton, Michael
;  TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
;  TITLE OF INVENTION:  Using an Inducible Gene Silencer
;  FILE REFERENCE: 01997.026400
;  CURRENT APPLICATION NUMBER: US/10/448,395
;  CURRENT FILING DATE:  2003-05-30
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 2133
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-1

  Query Match             100.0%;  Score 34;  DB 20;  Length 2133;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
                ||||||||||||||||||||||||||||||||||
Db        153 TACCGTTCGTATAGCATACATTATACGAAGTTAT 120


RESULT 15
US-10-214-722-7
; Sequence 7, Application US/10214722
; Publication No. US20030082723A1
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; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombinase-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-214-722-7

Query Match 95.3%; Score 32.4; DB 14; Length 34;
Best Local Similarity 97.1%; Pred. No. 0.0025;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              || |||||||||||||||||||||||||||||||
Db          1 TAGCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Search completed: September 8, 2005, 23:04:39
Job time : 310 secs

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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 22:19:49 ; Search time 1585.5 Seconds
(without alignments)
816.263 Million cell updates/sec

Title: US-10-030-658B-15
Perfect score: 34
Sequence: 1 taccgttcgtatagcatacattatacgaagttat 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	32.4	95.3	422	7	CF978723	CF978723 2-33-C10.
c	2	30.8	90.6	449	2	BF133141	BF133141 601645577
	3	30.8	90.6	575	7	CF975530	CF975530 2-97-F02.
	4	30.8	90.6	670	7	CF977704	CF977704 2-97-H02.
c	5	30.8	90.6	696	7	CF974915	CF974915 2-2-E01.R
c	6	30.8	90.6	739	8	AQ864471	AQ864471 nbeb0023G
c	7	30.8	90.6	810	8	AQ865062	AQ865062 nbeb0024N
c	8	30.8	90.6	896	2	BE748939	BE748939 601571869
c	9	30.8	90.6	1049	9	CL111198	CL111198 ISB1-54P4
	10	30	88.2	889	6	CB198925	CB198925 AGENCOURT
	11	30	88.2	910	7	CN385562	CN385562 LE2TR03P0
	12	29.4	86.5	235	7	CF979500	CF979500 2-97-A01.
c	13	29.4	86.5	441	8	AQ869026	AQ869026 nbeb0033I
c	14	29.4	86.5	452	8	AQ916088	AQ916088 nbeb0061K
c	15	29.4	86.5	633	8	AQ871906	AQ871906 nbeb0045C
c	16	29.4	86.5	771	8	AQ864951	AQ864951 nbeb0024B
c	17	29.4	86.5	802	8	AQ858133	AQ858133 nbeb0012E
c	18	29.4	86.5	826	8	AQ863178	AQ863178 nbeb0020B
	19	29.2	85.9	160	4	BG536159	BG536159 602564263
	20	29.2	85.9	385	6	CB354804	CB354804 ZF001-P00
c	21	29.2	85.9	443	5	BP626390	BP626390 BP626390
	22	29.2	85.9	562	6	CB352860	CB352860 ZF001-P00
c	23	29.2	85.9	849	8	B19733	B19733 F23L9-Sp6 I
c	24	29.2	85.9	904	9	CL140878	CL140878 ISB1-118B
c	25	29.2	85.9	1116	2	BE739791	BE739791 601556096
c	26	29.2	85.9	1153	9	CL101582	CL101582 ISB1-38M6
c	27	29	85.3	48	2	BF216440	BF216440 601884492
	28	29	85.3	56	2	BF571387	BF571387 602077548
	29	29	85.3	60	4	BG528528	BG528528 602580008
	30	29	85.3	64	4	BG425836	BG425836 602492160
	31	29	85.3	67	4	BF978473	BF978473 602148879
	32	29	85.3	69	4	BF978538	BF978538 602148767
	33	29	85.3	69	4	BG777209	BG777209 602664434
	34	29	85.3	70	4	BG401060	BG401060 602465124
	35	29	85.3	72	2	BF217647	BF217647 601883961
	36	29	85.3	74	2	BF692085	BF692085 602247861
	37	29	85.3	74	7	CO515863	CO515863 s13dSG87C
	38	29	85.3	75	2	BF692508	BF692508 602248039
	39	29	85.3	75	4	BG400894	BG400894 602464929
	40	29	85.3	75	4	BG501060	BG501060 602546471
	41	29	85.3	75	4	BG527937	BG527937 602556903
	42	29	85.3	75	4	BG542496	BG542496 602569575
	43	29	85.3	75	4	BG611824	BG611824 602613227
	44	29	85.3	75	4	BG612207	BG612207 602614192
	45	29	85.3	76	4	BG527897	BG527897 602556856

ALIGNMENTS

RESULT 1
CF978723
LOCUS CF978723 422 bp mRNA linear EST 24-JUN-2004
DEFINITION 2-33-C10.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA sequence.
ACCESSION CF978723
VERSION CF978723.1 GI:49174181
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 422)
AUTHORS Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
TITLE Gene Expression Profiling of Highly Purified Rat Retinal Ganglion Cells
JOURNAL Unpublished (2003)
COMMENT Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5230
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.
FEATURES Location/Qualifiers
source 1. .422
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="Retinal Ganglion Cells"
/lab_host="DH10B"
/clone_lib="Rat retinal ganglion cell"
/note="Organ: Eye; Vector: pDNR-LIB; Site_1: SfiI; Site_2: SfiI; The library was constructed from purified rat retinal ganglion cells. The Creator SMART cDNA Library method (Clontech) was used. EST analysis was performed on the unamplified, non-normalized, non-subtracted library."
ORIGIN

Query Match 95.3%; Score 32.4; DB 7; Length 422;
Best Local Similarity 97.1%; Pred. No. 0.0054;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db         17 TAACGTTCGTATAGCATACATTATACGAAGTTAT 50


RESULT 2
BF133141/c
LOCUS       BF133141                 449 bp    mRNA    linear   EST 24-OCT-2000
DEFINITION  601645577R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3930715 3',
            mRNA sequence.
ACCESSION   BF133141
VERSION     BF133141.1  GI:10972181
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 449)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM765  row: i  column: 20
            High quality sequence start: 3
            High quality sequence stop: 215.
FEATURES             Location/Qualifiers
     source          1. .449
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3930715"
                     /tissue_type="mucoepidermoid carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_59"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).  Average
                     insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 2;  Length 449;
  Best Local Similarity   94.1%;  Pred. No. 0.025;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              || | ||||||||||||||||||||||||||||||
Db         34 TAACCTTCGTATAGCATACATTATACGAAGTTAT 1


RESULT 3
CF975530
LOCUS       CF975530                 575 bp    mRNA    linear   EST 24-JUN-2004
DEFINITION  2-97-F02.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA
            sequence.
ACCESSION   CF975530
VERSION     CF975530.1  GI:49170988
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 575)
  AUTHORS   Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
  TITLE     Gene Expression Profiling of Highly Purified Rat Retinal Ganglion
            Cells
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Farkas RH
            Department of Ophthalmology
            Johns Hopkins University School of Medicine
            600 North Wolfe Street, Baltimore, MD 21287, USA
            Tel: 410 502 5230
            Fax: 410 502 5382
            Email: rfarkas@jhmi.edu.
FEATURES             Location/Qualifiers
     source          1. .575
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="Retinal Ganglion Cells"
                     /lab_host="DH10B"
                     /clone_lib="Rat retinal ganglion cell"
                     /note="Organ: Eye; Vector: pDNR-LIB; Site_1: SfiI; Site_2:
                     SfiI; The library was constructed from purified rat
                     retinal ganglion cells. The Creator SMART cDNA Library
                     method (Clontech) was used. EST analysis was performed on
                     the unamplified, non-normalized, non-subtracted library."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 7;  Length 575;
  Best Local Similarity   94.1%;  Pred. No. 0.026;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              |||  ||||||||||||||||||||||||||||||
Db         19 TACACTTCGTATAGCATACATTATACGAAGTTAT 52


RESULT 4
CF977704
LOCUS       CF977704                 670 bp    mRNA    linear   EST 24-JUN-2004
DEFINITION  2-97-H02.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA
            sequence.
ACCESSION   CF977704
VERSION     CF977704.1  GI:49173162
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 670)
  AUTHORS   Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
  TITLE     Gene Expression Profiling of Highly Purified Rat Retinal Ganglion
            Cells
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Farkas RH
            Department of Ophthalmology
            Johns Hopkins University School of Medicine
            600 North Wolfe Street, Baltimore, MD 21287, USA
            Tel: 410 502 5230
            Fax: 410 502 5382
            Email: rfarkas@jhmi.edu.
FEATURES             Location/Qualifiers
     source          1. .670
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="Retinal Ganglion Cells"
                     /lab_host="DH10B"
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                     /clone_lib="Rat retinal ganglion cell"
                     /note="Organ: Eye; Vector: pDNR-LIB; Site_1: SfiI; Site_2:
                     SfiI; The library was constructed from purified rat
                     retinal ganglion cells. The Creator SMART cDNA Library
                     method (Clontech) was used. EST analysis was performed on
                     the unamplified, non-normalized, non-subtracted library."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 7;  Length 670;
  Best Local Similarity   94.1%;  Pred. No. 0.026;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              || | ||||||||||||||||||||||||||||||
Db         22 TAACCTTCGTATAGCATACATTATACGAAGTTAT 55


RESULT 5
CF974915/c
LOCUS       CF974915                 696 bp    mRNA    linear   EST 24-JUN-2004
DEFINITION  2-2-E01.R Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA
            sequence.
ACCESSION   CF974915
VERSION     CF974915.1  GI:49170373
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
  TITLE     Gene Expression Profiling of Highly Purified Rat Retinal Ganglion
            Cells
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Farkas RH
            Department of Ophthalmology
            Johns Hopkins University School of Medicine
            600 North Wolfe Street, Baltimore, MD 21287, USA
            Tel: 410 502 5230
            Fax: 410 502 5382
            Email: rfarkas@jhmi.edu.
FEATURES             Location/Qualifiers
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                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="Retinal Ganglion Cells"
                     /lab_host="DH10B"
                     /clone_lib="Rat retinal ganglion cell"
                     /note="Organ: Eye; Vector: pDNR-LIB; Site_1: SfiI; Site_2:
                     SfiI; The library was constructed from purified rat
                     retinal ganglion cells. The Creator SMART cDNA Library
                     method (Clontech) was used. EST analysis was performed on
                     the unamplified, non-normalized, non-subtracted library."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 7;  Length 696;
  Best Local Similarity   94.1%;  Pred. No. 0.026;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              || | ||||||||||||||||||||||||||||||
Db        485 TAACCTTCGTATAGCATACATTATACGAAGTTAT 452


RESULT 6
AQ864471/c
LOCUS       AQ864471                 739 bp    DNA     linear   GSS 03-NOV-1999
DEFINITION  nbeb0023G19r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica
            cultivar-group) genomic clone nbeb0023G19r, genomic survey
            sequence.
ACCESSION   AQ864471
VERSION     AQ864471.1  GI:6214837
KEYWORDS    GSS.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 739)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: GGAAACAGCTATGACCATG
            Class: BAC ends
            High quality sequence start: 37
            High quality sequence stop: 512.
FEATURES             Location/Qualifiers
     source          1. .739
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="nbeb0023G19r"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /clone_lib="CUGI Rice BAC Library (EcoRI)"
                     /note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
                     Rice is the most important food crop in the world. Half of
                     the world population, especially those inhabiting highly
                     populated areas of the humid tropics and subtropics, rely
                     on rice as their primary source of carbohydrate.
                     Monocotyledonous rice is a diploid plant (2n=24) with a
                     haploid genome equivalent of 431 Mbp (Arumuganathan and
                     Earle, 1991). The relatively small genome of rice, three
                     times larger than that of Arabidopsis, makes it suitable
                     for genomic studies. In order to facilitate positional
                     cloning, physical mapping and genome sequencing of rice,
                     we have constructed a BAC library from Oryza sativa,
                     Nipponbare variety using EcoRI as the cloning enzyme. The
                     library contains 55,296 clones with an average insert size
                     of 121 Kb providing approximatley 15 haploid genome
                     equivalents. The deep coverage allows the isolation a
                     particular sequence with a probability of 99.9 %. Three
                     high density filters, each containing 18,432 clones
                     (doubly spotted), represent the whole library for colony
                     screening and can be requested from the Clemson University
                     BAC/EST Resource Center (www.genome.clemson.edu)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 8;  Length 739;
  Best Local Similarity   94.1%;  Pred. No. 0.026;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              || | ||||||||||||||||||||||||||||||
Db        441 TAACTTTCGTATAGCATACATTATACGAAGTTAT 408


RESULT 7
AQ865062/c
LOCUS       AQ865062                 810 bp    DNA     linear   GSS 03-NOV-1999
DEFINITION  nbeb0024N11r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica
            cultivar-group) genomic clone nbeb0024N11r, genomic survey
            sequence.
ACCESSION   AQ865062
VERSION     AQ865062.1  GI:6215519
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```
KEYWORDS    GSS.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 810)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: GGAAACAGCTATGACCATG
            Class: BAC ends
            High quality sequence start: 43
            High quality sequence stop: 360.
FEATURES             Location/Qualifiers
     source          1. .810
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="nbeb0024N11r"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /clone_lib="CUGI Rice BAC Library (EcoRI)"
                     /note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
                     Rice is the most important food crop in the world. Half of
                     the world population, especially those inhabiting highly
                     populated areas of the humid tropics and subtropics, rely
                     on rice as their primary source of carbohydrate.
                     Monocotyledonous rice is a diploid plant (2n=24) with a
                     haploid genome equivalent of 431 Mbp (Arumuganathan and
                     Earle, 1991). The relatively small genome of rice, three
                     times larger than that of Arabidopsis, makes it suitable
                     for genomic studies. In order to facilitate positional
                     cloning, physical mapping and genome sequencing of rice,
                     we have constructed a BAC library from Oryza sativa,
                     Nipponbare variety using EcoRI as the cloning enzyme. The
                     library contains 55,296 clones with an average insert size
                     of 121 Kb providing approximatley 15 haploid genome
                     equivalents. The deep coverage allows the isolation a
                     particular sequence with a probability of 99.9 %. Three
                     high density filters, each containing 18,432 clones
                     (doubly spotted), represent the whole library for colony
                     screening and can be requested from the Clemson University
                     BAC/EST Resource Center (www.genome.clemson.edu)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 8;  Length 810;
  Best Local Similarity   94.1%;  Pred. No. 0.026;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              |||| || ||||||||||||||||||||||||||
Db        449 TACCTTTGGTATAGCATACATTATACGAAGTTAT 416


RESULT 8
BE748939/c
LOCUS       BE748939                 896 bp    mRNA    linear   EST 15-SEP-2000
DEFINITION  601571869T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838936 3',
            mRNA sequence.
ACCESSION   BE748939
VERSION     BE748939.1  GI:10162931
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM526  row: i  column: 17
            High quality sequence start: 20
            High quality sequence stop: 268.
FEATURES             Location/Qualifiers
     source          1. .896
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3838936"
                     /tissue_type="from acute myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_55"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.65 kb (range 0.9-4.0 kb).  14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 2;  Length 896;
  Best Local Similarity   94.1%;  Pred. No. 0.026;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              || | ||||||||||||||||||||||||||||
Db         88 TAACCTTCGTATAGCATACATTATACGAAGTTAT 55


RESULT 9
CL111198/c
LOCUS       CL111198                 1049 bp    DNA     linear   GSS 05-JAN-2004
DEFINITION  ISB1-54P4_Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-54P4,
            genomic survey sequence.
ACCESSION   CL111198
VERSION     CL111198.1  GI:40604833
KEYWORDS    GSS.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 1049)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE     A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 75000   Std Error: 0.00
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```
          Seq primer: Sp6 ATTTAGGTGACACTATAG
          Class: BAC ends
          High quality sequence start: 116
          High quality sequence stop: 895.
FEATURES             Location/Qualifiers
     source          1. .1049
                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:8364"
                     /clone="ISB1-54P4"
                     /clone_lib="ISB1"
                     /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
                     Library Segment 1"
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 9;  Length 1049;
  Best Local Similarity   94.1%;  Pred. No. 0.026;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
              || | ||||||||||||||||||||||||||||||
Db        937 TAACTTTCGTATAGCATACATTATACGAAGTTAT 904


RESULT 10
CB198925
LOCUS       CB198925                889 bp    mRNA    linear   EST 21-MAR-2003
DEFINITION  AGENCOURT_11212397 NICHD_XGC_Tad2 Xenopus laevis cDNA clone
            IMAGE:6873929 5', mRNA sequence.
ACCESSION   CB198925
VERSION     CB198925.2  GI:29148851
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 889)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Feb 4, 2003 this sequence version replaced gi:28229700.
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Drs. Donald Brown and Liquan Cai
             cDNA Library Preparation: CLONTECH
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM3106  row: o  column: 16
            High quality sequence stop: 476.
FEATURES             Location/Qualifiers
     source          1. .889
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:6873929"
                     /dev_stage="metamorphosis stage 62"
                     /clone_lib="NICHD_XGC_Tad2"
                     /note="Organ: Developing Tadpole; Vector: pDNR-LIB;
                     Site_1: SfiI; Site_2: SfiI; 5' and 3' adaptors were used
                     in cloning as follows: 5' adaptor sequence:
                     5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.7 kb
                     (range 0.8-3.0 kb). 15/15 colonies contained inserts by
                     PCR. This library was enriched for full-length clones and
                     was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN

  Query Match             88.2%;  Score 30;  DB 6;  Length 889;
  Best Local Similarity   100.0%;  Pred. No. 0.056;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db          8 GTTCGTATAGCATACATTATACGAAGTTAT 37


RESULT 11
CN385562
LOCUS       CN385562                910 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  LE2TR03P06 Tomato CL5915 roots under different developmental stages
            Lycopersicon esculentum cDNA clone LE2TR03P06, mRNA sequence.
ACCESSION   CN385562
VERSION     CN385562.1  GI:51700876
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
            Insert Length: 910  Std Error: 0.00
            Plate: 03  row: P  column: 06
            Seq primer: smart2.
FEATURES             Location/Qualifiers
     source          1. .910
                     /organism="Lycopersicon esculentum"
                     /mol_type="mRNA"
                     /cultivar="CL5915"
                     /db_xref="taxon:4081"
                     /clone="LE2TR03P06"
                     /tissue_type="roots"
                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN

  Query Match             88.2%;  Score 30;  DB 7;  Length 910;
  Best Local Similarity   100.0%;  Pred. No. 0.056;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GTTCGTATAGCATACATTATACGAAGTTAT 34
              ||||||||||||||||||||||||||||||
Db        757 GTTCGTATAGCATACATTATACGAAGTTAT 786


RESULT 12
CF979500
LOCUS       CF979500                235 bp    mRNA    linear   EST 24-JUN-2004
DEFINITION  2-97-A01.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA
            sequence.
ACCESSION   CF979500
VERSION     CF979500.1  GI:49174961
```

```
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 235)
  AUTHORS   Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
  TITLE     Gene Expression Profiling of Highly Purified Rat Retinal Ganglion
            Cells
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Farkas RH
            Department of Ophthalmology
            Johns Hopkins University School of Medicine
            600 North Wolfe Street, Baltimore, MD 21287, USA
            Tel: 410 502 5230
            Fax: 410 502 5382
            Email: rfarkas@jhmi.edu.
FEATURES             Location/Qualifiers
     source          1. .235
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="Retinal Ganglion Cells"
                     /lab_host="DH10B"
                     /clone_lib="Rat retinal ganglion cell"
                     /note="Organ: Eye; Vector: pDNR-LIB; Site_1: SfiI; Site_2:
                     SfiI; The library was constructed from purified rat
                     retinal ganglion cells. The Creator SMART cDNA Library
                     method (Clontech) was used. EST analysis was performed on
                     the unamplified, non-normalized, non-subtracted library."
ORIGIN

  Query Match             86.5%;  Score 29.4;  DB 7;  Length 235;
  Best Local Similarity   96.8%;  Pred. No. 0.093;
  Matches   30;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGTTCGTATAGCATACATTATACGAAGTTAT 34
              | ||||||||||||||||||||||||||||||
Db         21 CCTTCGTATAGCATACATTATACGAAGTTAT 51


RESULT 13
AQ869026/c
LOCUS       AQ869026                441 bp    DNA     linear   GSS 03-NOV-1999
DEFINITION  nbeb0033I02r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica
            cultivar-group) genomic clone nbeb0033I02r, genomic survey
            sequence.
ACCESSION   AQ869026
VERSION     AQ869026.1  GI:6219477
KEYWORDS    GSS.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 441)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: GGAAACAGCTATGACCATG
            Class: BAC ends
            High quality sequence start: 35
            High quality sequence stop: 342.
FEATURES             Location/Qualifiers
     source          1. .441
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="nbeb0033I02r"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /clone_lib="CUGI Rice BAC Library (EcoRI)"
                     /note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
                     Rice is the most important food crop in the world. Half of
                     the world population, especially those inhabiting highly
                     populated areas of the humid tropics and subtropics, rely
                     on rice as their primary source of carbohydrate.
                     Monocotyledonous rice is a diploid plant (2n=24) with a
                     haploid genome equivalent of 431 Mbp (Arumuganathan and
                     Earle, 1991). The relatively small genome of rice, three
                     times larger than that of Arabidopsis, makes it suitable
                     for genomic studies. In order to facilitate positional
                     cloning, physical mapping and genome sequencing of rice,
                     we have constructed a BAC library from Oryza sativa,
                     Nipponbare variety using EcoRI as the cloning enzyme. The
                     library contains 55,296 clones with an average insert size
                     of 121 Kb providing approximatley 15 haploid genome
                     equivalents. The deep coverage allows the isolation a
                     particular sequence with a probability of 99.9 %. Three
                     high density filters, each containing 18,432 clones
                     (doubly spotted), represent the whole library for colony
                     screening and can be requested from the Clemson University
                     BAC/EST Resource Center (www.genome.clemson.edu)."
ORIGIN

  Query Match             86.5%;  Score 29.4;  DB 8;  Length 441;
  Best Local Similarity   96.8%;  Pred. No. 0.096;
  Matches   30;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGTTCGTATAGCATACATTATACGAAGTTAT 34
              | ||||||||||||||||||||||||||||||
Db        430 CCTTCGTATAGCATACATTATACGAAGTTAT 400


RESULT 14
AQ916088/c
LOCUS       AQ916088                452 bp    DNA     linear   GSS 02-DEC-1999
DEFINITION  nbeb0061K08r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica
            cultivar-group) genomic clone nbeb0061K08r, genomic survey
            sequence.
ACCESSION   AQ916088
VERSION     AQ916088.1  GI:6512604
KEYWORDS    GSS.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: GGAAACAGCTATGACCATG
            Class: BAC ends
            High quality sequence start: 31
            High quality sequence stop: 201.
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Oryza sativa (japonica cultivar-group)"
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbeb0061K08r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."

ORIGIN

Query Match 86.5%; Score 29.4; DB 8; Length 452;
Best Local Similarity 96.8%; Pred. No. 0.097;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db 427 CCTTCGTATAGCATACATTATACGAAGTTAT 397

RESULT 15
AQ871906/c
LOCUS AQ871906 633 bp DNA linear GSS 03-NOV-1999
DEFINITION nbeb0045C24r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica cultivar-group) genomic clone nbeb0045C24r, genomic survey sequence.
ACCESSION AQ871906
VERSION AQ871906.1 GI:6222357
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 633)
AUTHORS Wing,R.A. and Dean,R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 30
High quality sequence stop: 466.
FEATURES Location/Qualifiers
source 1. .633
/organism="Oryza sativa (japonica cultivar-group)"
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/db_xref="taxon:39947"
/clone="nbeb0045C24r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."

ORIGIN

Query Match 86.5%; Score 29.4; DB 8; Length 633;
Best Local Similarity 96.8%; Pred. No. 0.098;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGTTCGTATAGCATACATTATACGAAGTTAT 34
|||||||||||||||||||||||||||||||
Db 576 CCTTCGTATAGCATACATTATACGAAGTTAT 546

Search completed: September 9, 2005, 00:32:13
Job time : 1588.5 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 21:11:18 ; Search time 797 Seconds
(without alignments)
2067.098 Million cell updates/sec

Title: US-10-030-658B-16
Perfect score: 34
Sequence: 1 ataacttcgtatagcatacattatacgaacggta 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
3: gb_in:*
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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	34	100.0	34	6	BD182869	BD182869 Knockout
	2	34	100.0	34	6	BD185623	BD185623 Knockout
	3	34	100.0	34	6	AX114842	AX114842 Sequence
	4	34	100.0	34	6	AX137068	AX137068 Sequence
	5	34	100.0	34	6	AX540641	AX540641 Sequence
	6	34	100.0	34	6	AX710004	AX710004 Sequence
	7	34	100.0	34	6	BD083073	BD083073 Antisense
	8	34	100.0	34	6	BD093612	BD093612 Antisense
	9	34	100.0	44	6	AX710017	AX710017 Sequence
c	10	34	100.0	67	6	AX710015	AX710015 Sequence
	11	34	100.0	78	6	AX114851	AX114851 Sequence
c	12	34	100.0	79	6	AX114852	AX114852 Sequence
	13	34	100.0	94	6	AX662254	AX662254 Sequence
	14	34	100.0	94	6	AX662260	AX662260 Sequence
	15	34	100.0	7175	6	AX114853	AX114853 Sequence
	16	34	100.0	8153	6	AX114871	AX114871 Sequence
	17	34	100.0	8811	12	AY569779	AY569779 Cloning v
	18	34	100.0	9479	12	AY569778	AY569778 Cloning v
	19	34	100.0	12404	12	AY569780	AY569780 Cloning v
	20	32.4	95.3	34	6	AX710005	AX710005 Sequence
c	21	31.4	92.4	63339	2	AC101135	AC101135 Mus muscu
	22	30.8	90.6	34	6	AX710006	AX710006 Sequence
c	23	30.8	90.6	61583	2	AC100438	AC100438 Mus muscu
c	24	30.4	89.4	71206	2	AC027744	AC027744 Homo sapi
c	25	30	88.2	40	6	AX148779	AX148779 Sequence
c	26	30	88.2	151992	2	AC009939	AC009939 Homo sapi
	27	29.8	87.6	62556	2	AC125011	AC125011 Mus muscu
c	28	29.8	87.6	67119	2	AC100327	AC100327 Mus muscu
c	29	29.4	86.5	47673	2	AC083879	AC083879 Homo sapi
c	30	29.4	86.5	60911	2	AC111174	AC111174 Homo sapi
	31	29.4	86.5	65987	2	AC117992	AC117992 Mus muscu
	32	29.4	86.5	79649	2	AC026247	AC026247 Homo sapi
c	33	29.4	86.5	129851	2	AC027751	AC027751 Homo sapi
	34	29.4	86.5	147521	2	AC013680	AC013680 Homo sapi
	35	29.4	86.5	213913	2	AC027813	AC027813 Homo sapi
	36	29.2	85.9	34	6	AX710007	AX710007 Sequence
	37	29.2	85.9	722	6	AX823824	AX823824 Sequence
c	38	29.2	85.9	58483	2	AC100352	AC100352 Mus muscu
c	39	29.2	85.9	60186	2	AC126330	AC126330 Homo sapi
c	40	29.2	85.9	60481	2	AC099844	AC099844 Homo sapi
c	41	29.2	85.9	70203	2	AC024012	AC024012 Homo sapi
c	42	29.2	85.9	83775	2	AC022466	AC022466 Homo sapi
c	43	29.2	85.9	98011	2	AC138276	AC138276 Homo sapi
c	44	29.2	85.9	147201	2	AC013765	AC013765 Homo sapi
	45	29	85.3	29	6	AR535082	AR535082 Sequence

ALIGNMENTS

RESULT 1
BD182869
LOCUS BD182869 34 bp DNA linear PAT 17-JUN-2003
DEFINITION Knockout animal.
ACCESSION BD182869
VERSION BD182869.1 GI:31875069
KEYWORDS JP 2002345477-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 34)
AUTHORS Ide,H., Yamamura,K. and Araki,K.
TITLE Knockout animal
JOURNAL Patent: JP 2002345477-A 2 03-DEC-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA,
KIMI ARAKI
COMMENT OS Artificial Sequence
PN JP 2002345477-A/2
PD 03-DEC-2002
PF 25-MAY-2001 JP 2001157567
PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
Description of Artificial Sequence:synthetic DNA FH Key
Location/Qualifiers
FT source 1. .34
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .34
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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Db 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34

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RESULT 2
BD185623
LOCUS       BD185623                  34 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Knockout animal.
ACCESSION   BD185623
VERSION     BD185623.1  GI:31877823
KEYWORDS    JP 2002369689-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Ide,H., Yamamura,K. and Araki,K.
  TITLE     Knockout animal
  JOURNAL   Patent: JP 2002369689-A 2 24-DEC-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
            KUMAMOTO UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002369689-A/2
            PD   24-DEC-2002
            PF   25-MAY-2001 JP 2001157568
            PI   HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
            PC   C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
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              Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:32630"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0.0015;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 3
AX114842
LOCUS       AX114842                  34 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 2 from Patent WO0129208.
ACCESSION   AX114842
VERSION     AX114842.1  GI:14031784
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 2 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES              Location/Qualifiers
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0.0015;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 4
AX137068
LOCUS       AX137068                  34 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 2 from Patent EP1092768.
ACCESSION   AX137068
VERSION     AX137068.1  GI:14273413
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R. and von Melchner,H.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: EP 1092768-A 2 18-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; FrankGen Biotechnologie AG (DE)
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:32630"
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0.0015;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 5
AX540641
LOCUS       AX540641                  34 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 10 from Patent WO0240685.
ACCESSION   AX540641
VERSION     AX540641.1  GI:25273630
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Xin,H.B. and Kotlikoff,M.
  TITLE     Vectors for conditional gene inactivation
  JOURNAL   Patent: WO 0240685-A 10 23-MAY-2002;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES              Location/Qualifiers
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                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0.0015;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 6
AX710004
LOCUS       AX710004                  34 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from Patent EP1288295.
ACCESSION   AX710004
VERSION     AX710004.1  GI:29786615
KEYWORDS    .
SOURCE      synthetic construct
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  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Altmann,M., Neuhierl,B. and Hammerschmidt,W.
  TITLE     Use of mutated recognition sites for multiple successive recombina
            se-mediated recombinations in a genetic system
  JOURNAL   Patent: EP 1288295-A 1 05-MAR-2003;
            GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="Oligonukleotid lox 66 ohne flanks"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 34;
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  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 7
BD083073
LOCUS       BD083073                  34 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense type gene trap vector.
ACCESSION   BD083073
VERSION     BD083073.1  GI:22628683
KEYWORDS    JP 2001321174-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Taniguchi,K. and Karasawa,M.
  TITLE     Antisense type gene trap vector
  JOURNAL   Patent: JP 2001321174-A 3 20-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2001321174-A/3
            PD   20-NOV-2001
            PF   11-MAY-2000 JP 2000138938
            PI   KATSUMI TANIGUCHI,MIKA KARASAWA
            PC   C12N15/09,A01K67/027,C12N5/10//(C12N5/10,C12R1:91),C12N15/00,
            PC   C12N5/00,
            PC   (C12N5/00,C12R1:91)
            CC   Description of Artificial Sequence:lox66 sequence FH   Key
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ORIGIN

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  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 8
BD093612
LOCUS       BD093612                  34 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense gene trap vector.
ACCESSION   BD093612
VERSION     BD093612.1  GI:22639200
KEYWORDS    WO 0185973-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Taniguchi,M. and Karasawa,M.
  TITLE     Antisense gene trap vector
  JOURNAL   Patent: WO 0185973-A 3 15-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP,MASARU TANIGUCHI,MIKA KARASAWA
COMMENT     OS   Artificial Sequence
            PN   WO 0185973-A/3
            PD   15-NOV-2001
            PF   29-AUG-2000 WO 2000JP005824
            PR   11-MAY-2000 JP 00P   138938
            PI   MASARU TANIGUCHI,MIKA KARASAWA
            PC   C12N15/85,C12N5/10,A01K67/027//A61K48/00
            CC   Description of Artificial Sequence:lox66 sequence FH   Key
                 Location/Qualifiers.
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ORIGIN

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Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 9
AX710017
LOCUS       AX710017                  44 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 14 from Patent EP1288295.
ACCESSION   AX710017
VERSION     AX710017.1  GI:29786628
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Altmann,M., Neuhierl,B. and Hammerschmidt,W.
  TITLE     Use of mutated recognition sites for multiple successive recombina
            se-mediated recombinations in a genetic system
  JOURNAL   Patent: EP 1288295-A 14 05-MAR-2003;
            GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
FEATURES             Location/Qualifiers
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                     /note="Oligonukleotid lox 66 mit flanks"
ORIGIN

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Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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Db          6 ATAACTTCGTATAGCATACATTATACGAACGGTA 39


RESULT 10
AX710015/c
LOCUS       AX710015                  67 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 12 from Patent EP1288295.
ACCESSION   AX710015
VERSION     AX710015.1  GI:29786626
KEYWORDS    .
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Altmann,M., Neuhierl,B. and Hammerschmidt,W.
  TITLE     Use of mutated recognition sites for multiple successive recombina
            se-mediated recombinations in a genetic system
  JOURNAL   Patent: EP 1288295-A 12 05-MAR-2003;
            GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .67
                     /organism="synthetic construct"
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ORIGIN

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Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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RESULT 11
AX114851
LOCUS       AX114851                  78 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 11 from Patent WO0129208.
ACCESSION   AX114851
VERSION     AX114851.1  GI:14031793
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 11 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
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  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          5 ATAACTTCGTATAGCATACATTATACGAACGGTA 38


RESULT 12
AX114852/c
LOCUS       AX114852                  79 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 12 from Patent WO0129208.
ACCESSION   AX114852
VERSION     AX114852.1  GI:14031794
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 12 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .79
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer lox4"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         79 ATAACTTCGTATAGCATACATTATACGAACGGTA 46


RESULT 13
AX662254
LOCUS       AX662254                  94 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 10 from Patent WO02083889.
ACCESSION   AX662254
VERSION     AX662254.1  GI:29163153
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bigger,B.W., Tolmachov,O. and Coutelle,C.
  TITLE     Methods
  JOURNAL   Patent: WO 02083889-A 10 24-OCT-2002;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .94
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         10 ATAACTTCGTATAGCATACATTATACGAACGGTA 43


RESULT 14
AX662260
LOCUS       AX662260                  94 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 16 from Patent WO02083889.
ACCESSION   AX662260
VERSION     AX662260.1  GI:29163159
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bigger,B.W., Tolmachov,O. and Coutelle,C.
  TITLE     Methods
  JOURNAL   Patent: WO 02083889-A 16 24-OCT-2002;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .94
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
ORIGIN

  Query Match             100.0%;  Score 34;  DB 6;  Length 94;
```

```
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         10 ATAACTTCGTATAGCATACATTATACGAACGGTA 43


RESULT 15
AX114853
LOCUS       AX114853               7175 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 13 from Patent WO0129208.
ACCESSION   AX114853
VERSION     AX114853.1  GI:14031795
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
  TITLE     Conditional gene trapping construct for the disruption of genes
  JOURNAL   Patent: WO 0129208-A 13 26-APR-2001;
            ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .7175
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="vector pRK57SA-beta"
ORIGIN

  Query Match           100.0%;  Score 34;  DB 6;  Length 7175;
  Best Local Similarity   100.0%;  Pred. No. 0.00082;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db        446 ATAACTTCGTATAGCATACATTATACGAACGGTA 479


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Job time :  799 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 21:09:03 ; Search time 200.5 Seconds
(without alignments)
1003.846 Million cell updates/sec

Title: US-10-030-658B-16
Perfect score: 34
Sequence: 1 ataacttcgtatagcatacattatacgaacggta 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	34	100.0	34	5	AAD04916	Aad04916 Recombina
	2	34	100.0	34	6	ABN84176	Abn84176 LoxP righ
	3	34	100.0	34	6	ABA03776	Aba03776 Synthetic
	4	34	100.0	34	8	ABV75996	Abv75996 Modified
	5	34	100.0	34	8	ABZ20924	Abz20924 LoxP muta
	6	34	100.0	34	8	ABZ79445	Abz79445 Lox 66 DN
	7	34	100.0	34	9	ACC85308	Acc85308 Recombina
c	8	34	100.0	34	10	ADD13801	Add13801 Oligonucl
	9	34	100.0	34	10	ADD15150	Add15150 Variant l
	10	34	100.0	34	10	ABZ75320	Abz75320 Lox66 rel
	11	34	100.0	44	8	ABZ20935	Abz20935 Lox66 iso
c	12	34	100.0	67	8	ABZ20923	Abz20923 Lox66 and
	13	34	100.0	78	5	AAD04925	Aad04925 Primer lo
c	14	34	100.0	79	5	AAD04926	Aad04926 Primer lo
	15	34	100.0	94	8	ABV75994	Abv75994 OLIGO-F,
	16	34	100.0	94	8	ABV75989	Abv75989 Oligonucl
	17	34	100.0	7175	5	AAD04927	Aad04927 Vector pR
	18	34	100.0	8153	5	AAD04945	Aad04945 Plasmid p
	19	32.4	95.3	34	8	ABZ20925	Abz20925 LoxP muta
	20	30.8	90.6	34	8	ABZ20926	Abz20926 LoxP muta
	21	30.8	90.6	34	9	ACC85310	Acc85310 Recombina
c	22	30.4	89.4	37	6	AAD31540	Aad31540 loxB olig
c	23	30	88.2	40	4	AAH44859	Aah44859 PCR prime
	24	29.2	85.9	34	8	ABZ20927	Abz20927 LoxP muta
c	25	29.2	85.9	68	5	AAH20921	Aah20921 E. coli g
	26	29.2	85.9	722	9	ADA12883	Ada12883 cHS4 dime
	27	29	85.3	29	4	AAH41178	Aah41178 Bacteriop
c	28	29	85.3	29	7	ADL18608	Adl18608 LoxC2 sit
c	29	29	85.3	34	2	AAQ47238	Aaq47238 loxP sequ
	30	29	85.3	34	2	AAQ47239	Aaq47239 loxP sequ
c	31	29	85.3	34	2	AAQ94929	Aaq94929 Wild type
c	32	29	85.3	34	2	AAT42300	Aat42300 Bacteriop
c	33	29	85.3	34	2	AAT42299	Aat42299 Bacteriop
	34	29	85.3	34	2	AAT36911	Aat36911 E. coli p
c	35	29	85.3	34	2	AAT92195	Aat92195 Bacteriop
c	36	29	85.3	34	2	AAT90585	Aat90585 Lox p rec
c	37	29	85.3	34	2	AAV17069	Aav17069 Lox P1 se
c	38	29	85.3	34	2	AAX76189	Aax76189 Variant l
c	39	29	85.3	34	2	AAX61038	Aax61038 Yeast Lox
	40	29	85.3	34	2	AAX76039	Aax76039 5' to 3'
	41	29	85.3	34	2	AAX19902	Aax19902 Wild-type
	42	29	85.3	34	3	AAA58294	Aaa58294 Bacteriop
c	43	29	85.3	34	3	AAA58293	Aaa58293 Bacteriop
	44	29	85.3	34	3	AAZ58066	Aaz58066 Wild-type
c	45	29	85.3	34	3	AAZ58071	Aaz58071 Cre recom

ALIGNMENTS

RESULT 1
AAD04916
ID AAD04916 standard; DNA; 34 BP.
XX
AC AAD04916;
XX
DT 17-JUL-2001 (first entry)
XX
DE Recombinase recognition sequence (RRS), loxP site mutant (lox66) DNA.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; loxP site; mutant; ds.
XX
OS Enterobacteria phage P1.
OS Synthetic.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-EP010162.
XX
PR 16-OCT-1999; 99EP-00120592.
PR 27-OCT-1999; 99US-0162016P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI Kuehn R, Von Melchener H, Altschmied J;
XX
DR WPI; 2001-308486/32.
XX
PT New gene trapping construct capable of causing conditional mutations in
PT genes, comprises functional DNA segment inserted in sense or antisense
PT direction relative to gene to be trapped.
XX
PS Claim 4; Page 49; 78pp; English.
XX
CC The present invention relates to a conditional gene trapping construct
CC capable of causing conditional mutations in genes. The gene trapping
CC construct comprises two functional DNA segments, each being flanked by
CC two recombinase recognition sequences (RRSs) specific to site specific

CC recombinase which is capable of unidirectional inversion of double
CC standard DNA segment. One of the DNA segment (disruption cassette) is
CC inserted in antisense orientation relative to the transcriptional
CC orientation of the gene to be trapped. The other DNA segment (selection
CC cassette) is inserted in sense direction relative to the transcriptional
CC orientation of the gene to be trapped. The cell comprising the gene
CC trapping construct is useful for the identification and/or isolation of
CC genes. The transgenic organism comprising the gene trapping construct is
CC useful to study gene function at various developmental stages. The gene
CC trapping construct is useful for mutationally inactivating all cellular
CC genes. The present DNA sequence encodes recombinase recognition sequence,
CC loxP site mutant (lox66), which flanks the functional DNA segments of
CC gene trapping construct
XX
SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||||||||
Db 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 2
ABN84176
ID ABN84176 standard; DNA; 34 BP.
XX
AC ABN84176;
XX
DT 23-SEP-2002 (first entry)
XX
DE LoxP right element mutant.
XX
KW Gene inactivation; mutagenesis; vector; knockout animal;
KW transgenic animal; gene trapping; loxP; mutant; ss.
XX
OS Enterobacteria phage P1.
OS Synthetic.
XX
PN WO200240685-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-US043916.
XX
PR 16-NOV-2000; 2000US-0249200P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Xin H, Kotlikoff M;
XX
DR WPI; 2002-537342/57.
XX
PT Novel genetically engineered vector comprising gene trap cassette, and
PT mutational element cassette that is transcriptionally silent, but which
PT is activated by recombinase expression to disrupt expression of trapped
PT gene.
XX
PS Example 2; Page 35; 58pp; English.
XX
CC The present invention provides recombinant vectors and methods of using
CC the vectors in a high-throughput genetic system to rapidly generate
CC conditional and/or conventional knockout mutants, e.g. in mice, useful
CC for identifying and defining mammalian gene function in vivo. The methods
CC combine gene trapping, gene targetting, and site-specific recombination
CC techniques. The vectors comprise a transcriptionally silent mutational
CC element that is inserted within a gene in a target cell in a manner that
CC retains gene function, and which can be manipulated to inactivate the
CC gene when desired. The mutational element may be flanked by mutant LoxP
CC sites in a manner that produces a directional bias toward inversion of
CC the mutational sequence upon exposure to cre recombinase. Once inverted,
CC the mutational element is spliced into the trapped gene resulting in
CC expression of a reporter gene and premature termination of the endogenous
CC mRNA. Site-directed DNA integration is achieved using a pair of mutant
CC loxP sites, a right element (RE) mutant (present sequence) and a left
CC element (LE) mutant (see ABN84175). The mutant loxP system produces a
CC reaction biased toward an irreversible gene inversion. The method of the
CC invention facilitates investigation of the function of individual genes
CC by a rapid extension of the conditional knockout approach
XX
SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||||||||
Db 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 3
ABA03776
ID ABA03776 standard; DNA; 34 BP.
XX
AC ABA03776;
XX
DT 19-FEB-2002 (first entry)
XX
DE Synthetic lox66 sequence.
XX
KW lox66; gene therapy; gene targeting; gene trapping;
KW antisense RNA production; ds.
XX
OS Synthetic.
XX
PN WO200185973-A1.
XX
PD 15-NOV-2001.
XX
PF 29-AUG-2000; 2000WO-JP005824.
XX
PR 11-MAY-2000; 2000JP-00138938.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Taniguchi M, Karasawa M;
XX
DR WPI; 2002-055602/07.
XX
PT Antisense type gene trap vector, useful for gene therapy of diseases and
PT production of animal models for disease study, disrupts transcription of
PT specific gene.
XX
PS Claim 19; Page 43; 48pp; Japanese.
XX
CC The invention relates to a method for producing cells in which the
CC expression of a gene is disrupted. The cells are transformed with a gene
CC trap vector to give a trap clone having the vector inserted at a specific
CC mutation site of the target gene. The trap clone is then transformed with
CC a vector that inserts a promoter in the antisense direction of the gene,
CC enforcing transcription of antisense RNA. The method is useful for the
CC production of animal models for studying human diseases. It is also
CC useful as gene therapy for the treatment and prevention of diseases. The
CC present sequence is a lox66 sequence claimed in the specification
XX
SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||||||||

```
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 4
ABV75996
ID   ABV75996 standard; DNA; 34 BP.
XX
AC   ABV75996;
XX
DT   11-FEB-2003  (first entry)
XX
DE   Modified right element loxP site.
XX
KW   LoxP; phage P1; recombination; minicircle; gene therapy; mitochondria;
KW   mutant; ss.
XX
OS   Bacteriophage p1.
OS   Synthetic.
XX
PN   WO200283889-A2.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2002; 2002WO-GB001668.
XX
PR   10-APR-2001; 2001GB-00008968.
PR   05-OCT-2001; 2001US-0327029P.
XX
PA   (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI   Bigger BW,  Tolmachov O,  Coutelle C;
XX
DR   WPI; 2003-075546/07.
XX
PT   New cell capable of expressing an endonuclease, useful for producing a
PT   minicircle for mitochondrial gene therapy, comprises a parent plasmid
PT   capable of recombination to form a minicircle and a miniplasmid.
XX
PS   Disclosure; Fig 4; 70pp; English.
XX
CC   The present sequence is that of a right element (RE) loxP site in which
CC   the 5 nucleotides at the 3' end of loxP have been modified. The RE loxP
CC   site is used in the method of the invention for the production of a
CC   minicircle. In this method, a parent plasmid is provided which has a
CC   nucleic acid sequence flanked by recombination sites. The plasmid is
CC   exposed to an enzyme which causes recombination at the recombination
CC   sites, forming (i) a minicircle comprising the nucleic acid sequence and
CC   (ii) a miniplasmid comprising the remainder of the parent plasmid. One
CC   recombination site is modified at the 5' end such that its reaction with
CC   the enzyme is less efficient than the wild-type site, and the other
CC   recombination site is modified at the 3' end such that its reaction with
CC   the enzyme is less efficient than the wild-type site, both modified sites
CC   being located in the minicircle after recombination. This favours the
CC   formation of the minicircle. In a preferred embodiment, the enzyme is Cre
CC   recombinase and the recombination sites are loxP sites. The method is
CC   preferably carried out in a bacterium, especially Escherichia coli. The
CC   minicircle can be used for mitochondrial gene therapy
XX
SQ   Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 8;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.00023;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 5
ABZ20924
ID   ABZ20924 standard; DNA; 34 BP.
XX
AC   ABZ20924;
XX
DT   10-APR-2003  (first entry)
XX
DE   LoxP mutant with flanking sequence oligonucleotide #1.
XX
KW   Non-identical recognition sequence mutant; sequence-specific recombinase;
KW   recombination; antibiotic-resistance marker; loxP; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   DE10140030-C1.
XX
PD   19-DEC-2002.
XX
PF   16-AUG-2001; 2001DE-01040030.
XX
PR   16-AUG-2001; 2001DE-01040030.
XX
PA   (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI   Altmann M,  Neuhierl B,  Hammerschmidt W;
XX
DR   WPI; 2003-048025/05.
XX
PT   Method for performing multiple recombination events in a genetic system,
PT   useful e.g. for removing antibiotic resistance genes, uses mutant
PT   recombinase recognition sites.
XX
PS   Claim 3; Col 9; 10pp; German.
XX
CC   The present invention relates to the use of two non-identical recognition
CC   sequence mutants for a sequence-specific recombinase for performing two
CC   or more recombination events, mediated by the sequence-specific
CC   recombinase, in a single genetic system. The method is used to manipulate
CC   genetic systems (microbial, plant or animal) by site-specific
CC   recombination, e.g. to insert or remove DNA and most particularly to
CC   remove antibiotic-resistance markers. The present sequence was used to
CC   isolate the loxP coding sequence in the exemplification of the invention
XX
SQ   Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 8;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.00023;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 6
ABZ79445
ID   ABZ79445 standard; DNA; 34 BP.
XX
AC   ABZ79445;
XX
DT   23-MAY-2003  (first entry)
XX
DE   Lox 66 DNA # SEQ ID 2.
XX
KW   LoxP; lox 66; knockout mouse; vascularisation; embryonic stem cell;
KW   drug development; locus of crossing over; ds.
XX
OS   Synthetic.
XX
PN   JP2002369689-A.
XX
PD   24-DEC-2002.
XX
PF   25-MAY-2001; 2001JP-00157568.
XX
PR   25-MAY-2001; 2001JP-00157568.
```

XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (IDEH/) IDE H.
PA (YAMA/) YAMAMURA K.
PA (ARAK/) ARAKI Y.
XX
DR WPI; 2003-125824/12.
XX
PT Knockout mouse or embryonic stem cells with introduced trap vectors
PT containing a loxP sequence or a variant loxP sequence with disrupted gene
PT of sequence No. 7 of 1405 bases.
XX
PS Claim 5; Fig 4; 21pp; Japanese.
XX
CC The invention relates to a knockout mouse or embryonic stem cells with
CC introduced trap vectors containing a loxP sequence. The knockout animals
CC of the invention may be used in the analysis of genomic functions,
CC particularly for investigating the processes of vascularisation and the
CC development of drugs participating in such processes. The current
CC sequence represents lox 66
XX
SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 8; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||||||||
Db 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 7
ACC85308
ID ACC85308 standard; DNA; 34 BP.
XX
AC ACC85308;
XX
DT 18-SEP-2003 (first entry)
XX
DE Recombinase lox66 DNA recognition sequence.
XX
KW Vegetable plastid transformation; transgenic; recognition sequence;
KW plant; site-specific integration; nutrition; seed production;
KW chemical production; ds.
XX
OS Unidentified.
XX
PN WO2003054201-A1.
XX
PD 03-JUL-2003.
XX
PF 16-DEC-2002; 2002WO-EP014303.
XX
PR 20-DEC-2001; 2001DE-01063159.
XX
PA (SUNG-) SUNGENE GMBH & CO KGAA.
XX
PI Biesgen C;
XX
DR WPI; 2003-541820/51.
XX
PT Site-specific integration of DNA into plastid DNA, useful for making
PT transgenic plants used e.g. as food, by recombinase-mediated insertion.
XX
PS Disclosure; Page 35; 164pp; German.
XX
CC The present invention relates to a method for the site-specific
CC integration of a DNA sequence into the plastid DNA of a plant or its
CC derived cells. Transgenic plants in which a DNA sequence has been
CC integrated, also their cell cultures, organs, tissues etc. are useful in
CC human or animal nutrition, to produce seeds, and to produce
CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,
CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The
CC present sequence is a recognition sequence shown in the exemplification
CC of the invention
XX
SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||||||||
Db 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 8
ADD13801/c
ID ADD13801 standard; DNA; 34 BP.
XX
AC ADD13801;
XX
DT 01-JAN-2004 (first entry)
XX
DE Oligonucleotide lox66 DNA.
XX
KW library; transfection; humanized monoclonal antibody; antigen;
KW T cell receptor; primer; ss.
XX
OS Synthetic.
XX
PN EP1298207-A1.
XX
PD 02-APR-2003.
XX
PF 01-OCT-2001; 2001EP-00123596.
XX
PR 01-OCT-2001; 2001EP-00123596.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Breitling F, Moldenhauer G, Poustka A, Kuehlwein T;
XX
DR WPI; 2003-383833/37.
XX
PT Preparing library of protein-producing eukaryotic cells, useful for
PT producing humanized high-affinity antibodies, comprises introducing
PT specific recombination signals into chromosomal gene loci and integrating
PT a variety of DNA sequences.
XX
PS Example 7; Page 15; 75pp; German.
XX
CC This invention describes a novel method of preparing a library of protein
CC -producing eukaryotic cells comprising (a) introducing specific
CC recombination signals into one or two chromosomal gene loci, (b)
CC Expanding at least one of the modified cells, (c) Transfecting many
CC different DNA sequences, each flanked by recombination signals, into the
CC expanded cells and (d) Integrating the DNA sequences into the gene loci
CC on the basis of the recombination signals and the appropriate
CC recombinase. The resulting cells express different proteins, each from an
CC integrated DNA sequence and the proteins are bound to the cell surface.
CC The method is particularly used to produce libraries of humanized
CC monoclonal antibodies, for selection of those with affinity for
CC particular antigens and useful for diagnostic or therapeutic use.
CC Libraries of T cell receptors may also be prepared. The method produces
CC libraries of high diversity; provides easy, quick and automatable
CC selection from a large number of proteins, allows relatively simple
CC alteration of the expressed gene (e.g. fusion to other protein-coding
CC sequences), is suitable for large scale protein production and allows
CC simple verification and characterization of selected cell lines. The
CC method does not require incorporation of a resistance marker. This
CC sequence represents oligonucleotide lox66.
XX
SQ Sequence 34 BP; 10 A; 5 C; 6 G; 13 T; 0 U; 0 Other;

```
  Query Match           100.0%;  Score 34;  DB 10;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.00023;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAACGGTA 1


RESULT 9
ADD15150
ID   ADD15150 standard; DNA; 34 BP.
XX
AC   ADD15150;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Variant loxP DNA recombination site designated lox66 (SeqID 2).
XX
KW   loxP site; circular; transgenic; plant; non-replicating; transgene;
KW   growth regulant; insect resistance; fungal disease resistance;
KW   stress resistance; ss; lox66.
XX
OS   Unidentified.
XX
PN   US2003100077-A1.
XX
PD   29-MAY-2003.
XX
PF   20-SEP-2001; 2001US-00957660.
XX
PR   20-SEP-2001; 2001US-00957660.
XX
PA   (KORT/) KORTE J A.
PA   (LOWE/) LOWE B A.
XX
PI   Korte JA,  Lowe BA;
XX
DR   WPI; 2003-777313/73.
XX
PT   Preparing a non-replicating, circular nucleic acid molecule useful for
PT   transforming crop plants to add desirable trait such as herbicide
PT   resistance, by amplifying starting circular nucleic acid molecule.
XX
PS   Claim 11; SEQ ID NO 2; 66pp; English.
XX
CC   This invention relates to an in vitro method to create circular molecules
CC   for use in transformation for the generation of transgenic plants.
CC   Specifically, it refers to a preparing a non-replicating, circular
CC   nucleic acid molecule using a first non-mutagenizing oligonucleotide
CC   primer with a nucleic acid sequence complementary to a selected sequence
CC   of the starting circular DNA molecule. As such, the present invention
CC   describes a method useful for preparing a fertile transgenic plant
CC   derived from a dicotyledonous plant preferably soybean and the transgenic
CC   cell is from a monocotyledon, preferably maize. The transgene can be a
CC   plant growth regulant with a selectable phenotype that confers an
CC   advantageous trait, for example, insect resistance, bacterial or fungal
CC   disease resistance, enhanced nutrient utilisation or stress resistance.
CC   This oligonucleotide sequence is a variant of the wild type loxP DNA
CC   recombination site known as lox66, used in an exemplification of the
CC   invention.
XX
SQ   Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 34;  DB 10;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.00023;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 10
ABZ75320
ID   ABZ75320 standard; DNA; 34 BP.
XX
AC   ABZ75320;
XX
DT   29-APR-2003  (first entry)
XX
DE   Lox66 related sequence.
XX
KW   Lox66; knockout animal; Tubedown-1; genomic function analysis;
KW   organ development; ds.
XX
OS   Unidentified.
XX
PN   JP2002345477-A.
XX
PD   03-DEC-2002.
XX
PF   25-MAY-2001; 2001JP-00157567.
XX
PR   25-MAY-2001; 2001JP-00157567.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA   (IDEH/) IDE H.
PA   (YAMA/) YAMAMURA K.
PA   (ARAK/) ARAKI Y.
XX
DR   WPI; 2003-072475/07.
XX
PT   Knockout animals with introduced a trap vector containing a variant loxP
PT   with introduced variation in a part of sequence(s) of a spacer sequence,
PT   and reverse repetitive sequence 1 and/or 2.
XX
PS   Claim 4; Page 12; 22pp; Japanese.
XX
CC   The invention relates to novel knockout animals with the disrupted
CC   Tubedown-1 gene. The transgenic animals of the invention are useful for
CC   analysis of genomic functions, and establishment of an analytic system
CC   for the development of organs. The present sequence is related to Lox66
XX
SQ   Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 34;  DB 10;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 0.00023;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 11
ABZ20935
ID   ABZ20935 standard; DNA; 44 BP.
XX
AC   ABZ20935;
XX
DT   10-APR-2003  (first entry)
XX
DE   Lox66 isolation oligonucleotide.
XX
KW   Non-identical recognition sequence mutant; sequence-specific recombinase;
KW   recombination; antibiotic-resistance marker; lox66; lox71; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   DE10140030-C1.
XX
PD   19-DEC-2002.
XX
```

PF 16-AUG-2001; 2001DE-01040030.
XX
PR 16-AUG-2001; 2001DE-01040030.
XX
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI Altmann M, Neuhierl B, Hammerschmidt W;
XX
DR WPI; 2003-048025/05.
XX
PT Method for performing multiple recombination events in a genetic system,
PT useful e.g. for removing antibiotic resistance genes, uses mutant
PT recombinase recognition sites.
XX
PS Example; Fig 1; 10pp; German.
XX
CC The present invention relates to the use of two non-identical recognition
CC sequence mutants for a sequence-specific recombinase for performing two
CC or more recombination events, mediated by the sequence-specific
CC recombinase, in a single genetic system. The method is used to manipulate
CC genetic systems (microbial, plant or animal) by site-specific
CC recombination, e.g. to insert or remove DNA and most particularly to
CC remove antibiotic-resistance markers. The present sequence was used to
CC isolate the lox66 and lox71 coding sequences in the exemplification of
CC the invention
XX
SQ Sequence 44 BP; 14 A; 10 C; 6 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||||||||
Db 6 ATAACTTCGTATAGCATACATTATACGAACGGTA 39

RESULT 12
ABZ20923/c
ID ABZ20923 standard; DNA; 67 BP.
XX
AC ABZ20923;
XX
DT 10-APR-2003 (first entry)
XX
DE Lox66 and lox71 isolation oligonucleotide #2.
XX
KW Non-identical recognition sequence mutant; sequence-specific recombinase;
KW recombination; antibiotic-resistance marker; lox66; lox71; PCR; primer;
KW ss.
XX
OS Unidentified.
XX
PN DE10140030-C1.
XX
PD 19-DEC-2002.
XX
PF 16-AUG-2001; 2001DE-01040030.
XX
PR 16-AUG-2001; 2001DE-01040030.
XX
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI Altmann M, Neuhierl B, Hammerschmidt W;
XX
DR WPI; 2003-048025/05.
XX
PT Method for performing multiple recombination events in a genetic system,
PT useful e.g. for removing antibiotic resistance genes, uses mutant
PT recombinase recognition sites.
XX
PS Example; Col 6; 10pp; German.
XX
CC The present invention relates to the use of two non-identical recognition
CC sequence mutants for a sequence-specific recombinase for performing two
CC or more recombination events, mediated by the sequence-specific
CC recombinase, in a single genetic system. The method is used to manipulate
CC genetic systems (microbial, plant or animal) by site-specific
CC recombination, e.g. to insert or remove DNA and most particularly to
CC remove antibiotic-resistance markers. The present sequence was used to
CC isolate the lox66 and lox71 coding sequences in the exemplification of
CC the invention
XX
SQ Sequence 67 BP; 20 A; 15 C; 16 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 8; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||||||||
Db 43 ATAACTTCGTATAGCATACATTATACGAACGGTA 10

RESULT 13
AAD04925
ID AAD04925 standard; DNA; 78 BP.
XX
AC AAD04925;
XX
DT 17-JUL-2001 (first entry)
XX
DE Primer lox3 for synthesising DNA fragment with loxP mutant sites.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; loxP site; primer; ss.
XX
OS Enterobacteria phage P1.
OS Synthetic.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-EP010162.
XX
PR 16-OCT-1999; 99EP-00120592.
PR 27-OCT-1999; 99US-0162016P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI Kuehn R, Von Melchener H, Altschmied J;
XX
DR WPI; 2001-308486/32.
XX
PT New gene trapping construct capable of causing conditional mutations in
PT genes, comprises functional DNA segment inserted in sense or antisense
PT direction relative to gene to be trapped.
XX
PS Example 1; Page 18; 78pp; English.
XX
CC The present invention relates to a conditional gene trapping construct
CC capable of causing conditional mutations in genes. The gene trapping
CC construct comprises two functional DNA segments, each being flanked by
CC two recombinase recognition sequences (RRSs) specific to site specific
CC recombinase which is capable of unidirectional inversion of double
CC standard DNA segment. One of the DNA segment (disruption cassette) is
CC inserted in antisense orientation relative to the transcriptional
CC orientation of the gene to be trapped. The other DNA segment (selection
CC cassette) is inserted in sense direction relative to the transcriptional
CC orientation of the gene to be trapped. The cell comprising the gene
CC trapping construct is useful for the identification and/or isolation of
CC genes. The transgenic organism comprising the gene trapping construct is
CC useful to study gene function at various developmental stages. The gene

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CC   trapping construct is useful for mutationally inactivating all cellular
CC   genes. The present sequence is a primer lox3 which is used for
CC   synthesising a DNA fragment containing a lox66 and a lox71 Cre
CC   recombinase recognition mutant sites in opposite orientation. The primer
CC   is used for constructing the gene trap vector pRK57SA-beta
XX
SQ   Sequence 78 BP; 27 A; 14 C; 14 G; 23 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 5;  Length 78;
  Best Local Similarity  100.0%;  Pred. No. 0.00024;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          5 ATAACTTCGTATAGCATACATTATACGAACGGTA 38


RESULT 14
AAD04926/c
ID   AAD04926 standard; DNA; 79 BP.
XX
AC   AAD04926;
XX
DT   17-JUL-2001  (first entry)
XX
DE   Primer lox4 for synthesising DNA fragment with loxP mutant sites.
XX
KW   Gene trapping construct; conditional mutation; unidirectional inversion;
KW   recombinase recognition sequence; RRS; disruption cassette;
KW   selection cassette; transgenic organism; loxP site; primer; ss.
XX
OS   Enterobacteria phage P1.
OS   Synthetic.
XX
PN   WO200129208-A1.
XX
PD   26-APR-2001.
XX
PF   16-OCT-2000; 2000WO-EP010162.
XX
PR   16-OCT-1999;   99EP-00120592.
PR   27-OCT-1999;   99US-0162016P.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
PA   (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI   Kuehn R,  Von Melchener H,  Altschmied J;
XX
DR   WPI; 2001-308486/32.
XX
PT   New gene trapping construct capable of causing conditional mutations in
PT   genes, comprises functional DNA segment inserted in sense or antisense
PT   direction relative to gene to be trapped.
XX
PS   Example 1; Page 18-19; 78pp; English.
XX
CC   The present invention relates to a conditional gene trapping construct
CC   capable of causing conditional mutations in genes. The gene trapping
CC   construct comprises two functional DNA segments, each being flanked by
CC   two recombinase recognition sequences (RRSs) specific to site specific
CC   recombinase which is capable of unidirectional inversion of double
CC   standard DNA segment. One of the DNA segment (disruption cassette) is
CC   inserted in antisense orientation relative to the transcriptional
CC   orientation of the gene to be trapped. The other DNA segment (selection
CC   cassette) is inserted in sense direction relative to the transcriptional
CC   orientation of the gene to be trapped. The cell comprising the gene
CC   trapping construct is useful for the identification and/or isolation of
CC   genes. The transgenic organism comprising the gene trapping construct is
CC   useful to study gene function at various developmental stages. The gene
CC   trapping construct is useful for mutationally inactivating all cellular
CC   genes. The present sequence is a primer lox4 which is used for
CC   synthesising a DNA fragment containing a lox66 and a lox71 Cre
CC   recombinase recognition mutant sites in opposite orientation. The primer
CC   is used for constructing the gene trap vector pRK57SA-beta
XX
SQ   Sequence 79 BP; 24 A; 14 C; 14 G; 27 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 5;  Length 79;
  Best Local Similarity  100.0%;  Pred. No. 0.00024;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         79 ATAACTTCGTATAGCATACATTATACGAACGGTA 46


RESULT 15
ABV75994
ID   ABV75994 standard; DNA; 94 BP.
XX
AC   ABV75994;
XX
DT   11-FEB-2003  (first entry)
XX
DE   OLIGO-F, contains attP and attB sites for phage phi-C31 integrase.
XX
KW   AttP; attB; phage phi-C31; integrase; recombination; minicircle;
KW   gene therapy; mitochondria; ss.
XX
OS   Bacteriophage phi-C31.
OS   Synthetic.
XX
PN   WO200283889-A2.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2002; 2002WO-GB001668.
XX
PR   10-APR-2001; 2001GB-00008968.
PR   05-OCT-2001; 2001US-0327029P.
XX
PA   (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI   Bigger BW,  Tolmachov O,  Coutelle C;
XX
DR   WPI; 2003-075546/07.
XX
PT   New cell capable of expressing an endonuclease, useful for producing a
PT   minicircle for mitochondrial gene therapy, comprises a parent plasmid
PT   capable of recombination to form a minicircle and a miniplasmid.
XX
PS   Example 3; Page 46; 70pp; English.
XX
CC   The present sequence is that of oligonucleotide OLIGO-F, which was
CC   annealed to OLIGO-R (see ABV75995) and introduced into plasmid pBC-SK(+),
CC   thereby creating attP and attB recombination sites. Minicircle-producing
CC   plasmids with attP and attB sites for phage phi-C31 integrase were
CC   constructed. This is an example of a method of the invention for the
CC   production of a minicircle. In this method, a plasmid having a DNA
CC   sequence flanked by attP and attB sites is exposed to phi-C31 integrase,
CC   thereby forming a minicircle comprising the DNA sequence and a
CC   miniplasmid comprising the remainder of the plasmid. The minicircle is
CC   useful for mitochondrial gene therapy
XX
SQ   Sequence 94 BP; 33 A; 19 C; 15 G; 27 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 34;  DB 8;  Length 94;
  Best Local Similarity  100.0%;  Pred. No. 0.00025;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         10 ATAACTTCGTATAGCATACATTATACGAACGGTA 43


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Job time : 201.5 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 19:07:03 ; Search time 69 Seconds
(without alignments)
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Perfect score: 34
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		29	85.3	29	4	US-09-662-128A-5	Sequence 5, Appli
2	c	29	85.3	34	1	US-08-214-023-1	Sequence 1, Appli
3		29	85.3	34	1	US-08-214-023-2	Sequence 2, Appli
4		29	85.3	34	1	US-08-615-048-1	Sequence 1, Appli
5		29	85.3	34	2	US-08-864-224-12	Sequence 12, Appl
6	c	29	85.3	34	2	US-08-864-224-17	Sequence 17, Appl
7	c	29	85.3	34	2	US-08-743-796-1	Sequence 1, Appli
8	c	29	85.3	34	2	US-08-350-260A-1	Sequence 1, Appli
9	c	29	85.3	34	2	US-08-350-260A-601	Sequence 601, App
10	c	29	85.3	34	3	US-08-654-623-4	Sequence 4, Appli
11	c	29	85.3	34	3	US-09-011-257-1	Sequence 1, Appli
12	c	29	85.3	34	3	US-08-412-777-1	Sequence 1, Appli
13	c	29	85.3	34	3	US-08-412-777-2	Sequence 2, Appli
14	c	29	85.3	34	3	US-08-412-826-1	Sequence 1, Appli
15	c	29	85.3	34	3	US-08-412-826-2	Sequence 2, Appli
16		29	85.3	34	3	US-09-214-471-1	Sequence 1, Appli
17		29	85.3	34	3	US-09-193-475-1	Sequence 1, Appli
18	c	29	85.3	34	3	US-09-563-239-1	Sequence 1, Appli
19	c	29	85.3	34	3	US-09-271-055A-1	Sequence 1, Appli
20	c	29	85.3	34	3	US-09-271-055A-2	Sequence 2, Appli
21	c	29	85.3	34	3	US-09-603-663-1	Sequence 1, Appli
22	c	29	85.3	34	3	US-09-603-663-3	Sequence 3, Appli
23		29	85.3	34	3	US-09-603-663-5	Sequence 5, Appli
24	c	29	85.3	34	3	US-09-603-658-1	Sequence 1, Appli
25	c	29	85.3	34	3	US-09-603-658-3	Sequence 3, Appli
26		29	85.3	34	3	US-09-603-658-5	Sequence 5, Appli
27	c	29	85.3	34	3	US-09-602-373A-1	Sequence 1, Appli
28	c	29	85.3	34	3	US-09-602-373A-3	Sequence 3, Appli
29		29	85.3	34	3	US-09-602-373A-5	Sequence 5, Appli
30		29	85.3	34	3	US-09-661-364-1	Sequence 1, Appli
31	c	29	85.3	34	3	US-09-610-259-1	Sequence 1, Appli
32	c	29	85.3	34	3	US-09-610-259-2	Sequence 2, Appli
33	c	29	85.3	34	3	US-09-554-271A-1	Sequence 1, Appli
34	c	29	85.3	34	3	US-09-837-863-1	Sequence 1, Appli
35	c	29	85.3	34	4	US-09-104-337A-1	Sequence 1, Appli
36	c	29	85.3	34	4	US-09-293-303-1	Sequence 1, Appli
37	c	29	85.3	34	4	US-09-718-034-2	Sequence 2, Appli
38	c	29	85.3	34	4	US-09-606-323C-1	Sequence 1, Appli
39	c	29	85.3	34	4	US-09-606-323C-3	Sequence 3, Appli
40	c	29	85.3	34	4	US-09-703-399A-1	Sequence 1, Appli
41	c	29	85.3	34	4	US-09-703-399A-3	Sequence 3, Appli
42		29	85.3	34	4	US-09-703-399A-5	Sequence 5, Appli
43		29	85.3	34	4	US-09-377-885A-1	Sequence 1, Appli
44	c	29	85.3	34	4	US-09-377-885A-20	Sequence 20, Appl
45		29	85.3	34	4	US-09-975-304-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-662-128A-5
; Sequence 5, Application US/09662128A
; Patent No. 6734295
; GENERAL INFORMATION:
; APPLICANT: MIYAGAWA, SHUJI
; APPLICANT: OKABE, MASARU
; TITLE OF INVENTION: MODIFIED CRE RECOMBINASE GENE FOR MAMMALS
; FILE REFERENCE: 197330US0
; CURRENT APPLICATION NUMBER: US/09/662,128A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: JP11-264364
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
US-09-662-128A-5

Query Match 85.3%; Score 29; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAA 29
||||||||||||||||||||||||||||
Db 1 ATAACTTCGTATAGCATACATTATACGAA 29

RESULT 2
US-08-214-023-1/c
; Sequence 1, Application US/08214023
; Patent No. 5434066
; GENERAL INFORMATION:
; APPLICANT: BEBEE, ROBERT L
; APPLICANT: HARTLEY, JAMES L
; TITLE OF INVENTION: MODULATION OF ENZYME ACTIVITIES IN THE
; TITLE OF INVENTION: IN VIVO CLONING OF DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEIL, GOTSHAL & MANGES
; STREET: 1615 L STREET, N.W.; SUITE 700
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.

```
;       ZIP:  20036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/214,023
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/862,188
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  AUERBACH, JEFFREY I
;       REGISTRATION NUMBER:  32,680
;       REFERENCE/DOCKET NUMBER:  59452.0011
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 682-7033
;       TELEFAX:  (202) 859-0939
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  34 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  ESCHERICHIA COLI
;       STRAIN:  DH1OB
US-08-214-023-1

  Query Match             85.3%;  Score 29;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              ||||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 3
US-08-214-023-2
; Sequence 2, Application US/08214023
; Patent No. 5434066
;  GENERAL INFORMATION:
;    APPLICANT:  BEBEE, ROBERT L
;    APPLICANT:  HARTLEY, JAMES L
;    TITLE OF INVENTION:  MODULATION OF ENZYME ACTIVITIES IN THE
;    TITLE OF INVENTION:  IN VIVO CLONING OF DNA
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WEIL, GOTSHAL & MANGES
;      STREET:  1615 L STREET, N.W.; SUITE 700
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/214,023
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/862,188
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  AUERBACH, JEFFREY I
;      REGISTRATION NUMBER:  32,680
;      REFERENCE/DOCKET NUMBER:  59452.0011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 682-7033
;      TELEFAX:  (202) 859-0939
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  ESCHERICHIA COLI
;      STRAIN:  DH1OB
US-08-214-023-2

  Query Match             85.3%;  Score 29;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              ||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAA 29


RESULT 4
US-08-615-048-1
; Sequence 1, Application US/08615048
; Patent No. 5700470
;  GENERAL INFORMATION:
;    APPLICANT:  Saito, Izumu
;    APPLICANT:  Kanegae, Yumi
;    APPLICANT:  Nakai, Michio
;    TITLE OF INVENTION:  RECOMBINANT DNA VIRUS AND METHOD FOR
;    TITLE OF INVENTION:  PREPARATION THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/615,048
;      FILING DATE:  12-MAR-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nakamura, Dean H.
;      REGISTRATION NUMBER:  33,981
;      REFERENCE/DOCKET NUMBER:  Q-41057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-615-048-1

  Query Match             85.3%;  Score 29;  DB 1;  Length 34;
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  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              ||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAA 29


RESULT 5
US-08-864-224-12
; Sequence 12, Application US/08864224
; Patent No. 5851808
;  GENERAL INFORMATION:
;    APPLICANT:  Elledge, Stephen J.
;    APPLICANT:  Liu, Qinghua
;    TITLE OF INVENTION:  Rapid Subcloning Using Site-Specific
;    TITLE OF INVENTION:  Recombination
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,224
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  BCM-02681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "DNA"
US-08-864-224-12

  Query Match             85.3%;  Score 29;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              ||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAA 29


RESULT 6
US-08-864-224-17/c
; Sequence 17, Application US/08864224
; Patent No. 5851808
;  GENERAL INFORMATION:
;    APPLICANT:  Elledge, Stephen J.
;    APPLICANT:  Liu, Qinghua
;    TITLE OF INVENTION:  Rapid Subcloning Using Site-Specific
;    TITLE OF INVENTION:  Recombination
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/864,224
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  BCM-02681
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "DNA"
US-08-864-224-17

  Query Match             85.3%;  Score 29;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              ||||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 7
US-08-743-796-1/c
; Sequence 1, Application US/08743796
; Patent No. 5928914
;  GENERAL INFORMATION:
;    APPLICANT:  Leboulch, P. et al.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TRANSFORMING CELLS
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/743,796
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane E. Remillard
;      REGISTRATION NUMBER:  38,872
;      REFERENCE/DOCKET NUMBER:  MTE-198
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-743-796-1

  Query Match             85.3%;  Score 29;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              |||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 8
US-08-350-260A-1/c
; Sequence 1, Application US/08350260A
; Patent No. 5962255
;  GENERAL INFORMATION:
;    APPLICANT:  Winter, Gregory Paul
;    APPLICANT:  Griffiths, Andrew David
;    APPLICANT:  Williams, Samuel Cameron
;    APPLICANT:  Waterhouse, Peter
;    APPLICANT:  Nissim, Ahuva
;    APPLICANT:  Johnson, Kevin Stuart
;    APPLICANT:  Smith, Andrew John Hammond
;    TITLE OF INVENTION:  Methods for producing members of specific
;    TITLE OF INVENTION:  binding pairs
;    NUMBER OF SEQUENCES:  602
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough
;      STREET:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/350,260A
;      FILING DATE:  05-DEC-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9110549.4
;      FILING DATE:  15-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB91/01134
;      FILING DATE:  10-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/00605
;      FILING DATE:  24-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/150,002
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/307,619
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/32372
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
US-08-350-260A-1

  Query Match             85.3%;  Score 29;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              |||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 9
US-08-350-260A-601/c
; Sequence 601, Application US/08350260A
; Patent No. 5962255
;  GENERAL INFORMATION:
;    APPLICANT:  Winter, Gregory Paul
;    APPLICANT:  Griffiths, Andrew David
;    APPLICANT:  Williams, Samuel Cameron
;    APPLICANT:  Waterhouse, Peter
;    APPLICANT:  Nissim, Ahuva
;    APPLICANT:  Johnson, Kevin Stuart
;    APPLICANT:  Smith, Andrew John Hammond
;    TITLE OF INVENTION:  Methods for producing members of specific
;    TITLE OF INVENTION:  binding pairs
;    NUMBER OF SEQUENCES:  602
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough
;      STREET:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/350,260A
;      FILING DATE:  05-DEC-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9110549.4
;      FILING DATE:  15-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB91/01134
;      FILING DATE:  10-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/00605
;      FILING DATE:  24-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/150,002
;      FILING DATE:  31-MAR-1994
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/307,619
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/32372
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  601:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-350-260A-601

  Query Match             85.3%;  Score 29;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              |||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 10
US-08-654-623-4/c
; Sequence 4, Application US/08654623
; Patent No. 6010884
;  GENERAL INFORMATION:
;    APPLICANT:  Griffiths, Andrew D
;    APPLICANT:  Holliger, Kaspar-Philipp
;    APPLICANT:  Nissim, Ahuva
;    APPLICANT:  Fisch, Igor
;    APPLICANT:  Winter, Gregory P
;    TITLE OF INVENTION:  Recombinant Binding Proteins and Peptides
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/654,623
;      FILING DATE:  29-MAY-1996
;      CLASSIFICATION:  435
;      CLASSIFICATION:  (C12N 1/21, C12R 1:19)
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9225453.1
;      FILING DATE:  04-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9300816.7
;      FILING DATE:  16-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93303614.7
;      FILING DATE:  10-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9319969.3
;      FILING DATE:  22-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/02492
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9412147.2
;      FILING DATE:  17-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/02662
;      FILING DATE:  05-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/448,418
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33259
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  Other nucleic acid: plasmid DNA
US-08-654-623-4

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              |||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 11
US-09-011-257-1/c
; Sequence 1, Application US/09011257
; Patent No. 6066478
; GENERAL INFORMATION:
;  APPLICANT: LUSKY, Monika
;  APPLICANT: MEHTALI, Majid
;  TITLE OF INVENTION: HELPER VIRUSES FOR PREPARING RECOMBINANT VIRAL VECTORS
;  FILE REFERENCE: 017753-090
;  CURRENT APPLICATION NUMBER: US/09/011,257
;  CURRENT FILING DATE: 1998-03-09
;  EARLIER APPLICATION NUMBER: FR 95/09.289
;  EARLIER FILING DATE: 1995-07-31
;  EARLIER APPLICATION NUMBER: PCT/FR96/01200
;  EARLIER FILING DATE: 1996-07-30
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Bacteriophage P1
US-09-011-257-1

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              |||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 12
US-08-412-777-1/c
; Sequence 1, Application US/08412777
; Patent No. 6091001
;  GENERAL INFORMATION:
;    APPLICANT:  JAKOBOVITS, AYA
;    APPLICANT:  ZSEBO, KRISZTINA M.
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES USING
;    TITLE OF INVENTION:  CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  CELL GENESYS, INC.
;      STREET:  322 LAKESIDE DRIVE
;      CITY:  FOSTER CITY
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/412,777
;      FILING DATE:  29-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDEL, SARALYNN
;      REGISTRATION NUMBER:  31,853
;      REFERENCE/DOCKET NUMBER:  CELL20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)358-9600 X345
;      TELEFAX:  (415)349-7392
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-412-777-1

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              ||||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 13
US-08-412-777-2/c
; Sequence 2, Application US/08412777
; Patent No. 6091001
;  GENERAL INFORMATION:
;    APPLICANT:  JAKOBOVITS, AYA
;    APPLICANT:  ZSEBO, KRISZTINA M.
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES USING
;    TITLE OF INVENTION:  CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CELL GENESYS, INC.
;      STREET:  322 LAKESIDE DRIVE
;      CITY:  FOSTER CITY
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/412,777
;      FILING DATE:  29-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDEL, SARALYNN
;      REGISTRATION NUMBER:  31,853
;      REFERENCE/DOCKET NUMBER:  CELL20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)358-9600 X345
;      TELEFAX:  (415)349-7392
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-412-777-2

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              ||||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 14
US-08-412-826-1/c
; Sequence 1, Application US/08412826
; Patent No. 6130364
;  GENERAL INFORMATION:
;    APPLICANT:  JAKOBOVITS, AYA
;    APPLICANT:  ZSEBO, KRISZTINA M.
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES USING
;    TITLE OF INVENTION:  CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CELL GENESYS, INC.
;      STREET:  322 LAKESIDE DRIVE
;      CITY:  FOSTER CITY
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/412,826
;      FILING DATE:  29-MAR-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDEL, SARALYNN
;      REGISTRATION NUMBER:  31,853
;      REFERENCE/DOCKET NUMBER:  CELL21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)358-9600 X345
;      TELEFAX:  (415)349-7392
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-412-826-1

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              ||||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


RESULT 15
US-08-412-826-2/c
; Sequence 2, Application US/08412826
; Patent No. 6130364
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;  GENERAL INFORMATION:
;    APPLICANT:  JAKOBOVITS, AYA
;    APPLICANT:  ZSEBO, KRISZTINA M.
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES USING
;    TITLE OF INVENTION:  CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CELL GENESYS, INC.
;      STREET:  322 LAKESIDE DRIVE
;      CITY:  FOSTER CITY
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/412,826
;      FILING DATE:  29-MAR-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDEL, SARALYNN
;      REGISTRATION NUMBER:  31,853
;      REFERENCE/DOCKET NUMBER:  CELL21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)358-9600 X345
;      TELEFAX:  (415)349-7392
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-412-826-2

  Query Match             85.3%;  Score 29;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAA 29
              ||||||||||||||||||||||||||||
Db         34 ATAACTTCGTATAGCATACATTATACGAA 6


Search completed: September  8, 2005, 21:11:10
Job time : 69 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 20:55:38 ; Search time 309 Seconds
(without alignments)
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Title: US-10-030-658B-16
Perfect score: 34
Sequence: 1 ataacttcgtatagcatacattatacgaacggta 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	34	100.0	34	10	US-09-957-660-2	Sequence 2, Appli
	2	34	100.0	34	14	US-10-118-231-18	Sequence 18, Appl
	3	34	100.0	34	14	US-10-214-722-1	Sequence 1, Appli
	4	34	100.0	34	18	US-10-416-995-10	Sequence 10, Appl
	5	34	100.0	34	19	US-10-739-769-2	Sequence 2, Appli
	6	34	100.0	34	20	US-10-448-395-8	Sequence 8, Appli
c	7	34	100.0	34	20	US-10-448-395-14	Sequence 14, Appl
c	8	34	100.0	40	20	US-10-448-395-17	Sequence 17, Appl
	9	34	100.0	40	20	US-10-448-395-18	Sequence 18, Appl
	10	34	100.0	44	14	US-10-214-722-14	Sequence 14, Appl
c	11	34	100.0	67	14	US-10-214-722-12	Sequence 12, Appl
c	12	34	100.0	75	22	US-10-916-082-10	Sequence 10, Appl
	13	34	100.0	94	14	US-10-118-231-10	Sequence 10, Appl
	14	34	100.0	94	14	US-10-118-231-16	Sequence 16, Appl
c	15	34	100.0	102	22	US-10-916-082-12	Sequence 12, Appl
	16	34	100.0	2133	20	US-10-448-395-1	Sequence 1, Appli
	17	32.4	95.3	34	14	US-10-214-722-2	Sequence 2, Appli
	18	30.8	90.6	34	14	US-10-214-722-3	Sequence 3, Appli
c	19	30.8	90.6	34	19	US-10-739-769-6	Sequence 6, Appli
	20	29.2	85.9	34	14	US-10-214-722-4	Sequence 4, Appli
c	21	29	85.3	34	9	US-09-829-507-1	Sequence 1, Appli
c	22	29	85.3	34	9	US-09-829-507-2	Sequence 2, Appli
c	23	29	85.3	34	9	US-09-920-932-1	Sequence 1, Appli
c	24	29	85.3	34	9	US-09-908-305-3	Sequence 3, Appli
	25	29	85.3	34	9	US-09-908-305-4	Sequence 4, Appli
	26	29	85.3	34	9	US-09-804-653-4	Sequence 4, Appli
c	27	29	85.3	34	9	US-09-804-653-6	Sequence 6, Appli
	28	29	85.3	34	9	US-09-822-634-3	Sequence 3, Appli
c	29	29	85.3	34	9	US-09-945-952A-4	Sequence 4, Appli
c	30	29	85.3	34	10	US-09-948-193-3	Sequence 3, Appli
	31	29	85.3	34	10	US-09-377-885A-1	Sequence 1, Appli
c	32	29	85.3	34	10	US-09-377-885A-20	Sequence 20, Appl
	33	29	85.3	34	10	US-09-981-397A-6	Sequence 6, Appli
c	34	29	85.3	34	10	US-09-997-209-29	Sequence 29, Appl
	35	29	85.3	34	10	US-09-990-185-7	Sequence 7, Appli
	36	29	85.3	34	10	US-09-957-660-1	Sequence 1, Appli
	37	29	85.3	34	10	US-09-957-660-4	Sequence 4, Appli
	38	29	85.3	34	10	US-09-975-304-1	Sequence 1, Appli
c	39	29	85.3	34	10	US-09-843-150-52	Sequence 52, Appl
c	40	29	85.3	34	10	US-09-843-150-53	Sequence 53, Appl
c	41	29	85.3	34	13	US-10-072-047-1	Sequence 1, Appli
c	42	29	85.3	34	13	US-10-072-047-2	Sequence 2, Appli
c	43	29	85.3	34	13	US-10-057-050-2	Sequence 2, Appli
c	44	29	85.3	34	14	US-10-081-771-1	Sequence 1, Appli
c	45	29	85.3	34	14	US-10-081-771-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-957-660-2
; Sequence 2, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; APPLICANT: LOWE, BRENDA A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; TITLE OF INVENTION: TRANSFORMATION
; FILE REFERENCE: DEKM:176US
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-957-660-2

Query Match 100.0%; Score 34; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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Db 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34

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RESULT 2
US-10-118-231-18
; Sequence 18, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
;  APPLICANT: Bigger, Brian W
;  APPLICANT:  Tolmachov, Oleg
;  APPLICANT:  Coutelle, Charles
;  TITLE OF INVENTION: Methods
;  FILE REFERENCE: 102286.141US
;  CURRENT APPLICATION NUMBER: US/10/118,231
;  CURRENT FILING DATE:  2002-04-09
;  PRIOR APPLICATION NUMBER: US 60/327,029
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: GB 0108968.9
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Construct
US-10-118-231-18

  Query Match             100.0%;  Score 34;  DB 14;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.00058;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 3
US-10-214-722-1
; Sequence 1, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
;  APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
;  TITLE OF INVENTION: The use of mutated recognition sequences for multiple
;  TITLE OF INVENTION:  consecutive recombinase-mediated recombinations
;  TITLE OF INVENTION:  in a genetic system
;  FILE REFERENCE: P14567
;  CURRENT APPLICATION NUMBER: US/10/214,722
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: DE 101 40 030.6
;  PRIOR FILING DATE: 2001-08-16
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence:
;   OTHER INFORMATION: Oligonucleotide lox 66 without flanks
US-10-214-722-1

  Query Match             100.0%;  Score 34;  DB 14;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.00058;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 4
US-10-416-995-10
; Sequence 10, Application US/10416995
; Publication No. US20040077089A1
; GENERAL INFORMATION:
;  APPLICANT: Xin, Hong-Bo
;  APPLICANT:  Kotlikoff, Michael
;  APPLICANT:  Cornell Research Foundation, Inc.
;  TITLE OF INVENTION: VECTORS FOR CONDITIONAL GENE INACTIVATION
;  FILE REFERENCE: 1153.020US1
;  CURRENT APPLICATION NUMBER: US/10/416,995
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: PCT/US01/43916
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: US 60/249,200
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A mutant loxP sequence
US-10-416-995-10

  Query Match             100.0%;  Score 34;  DB 18;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.00058;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 5
US-10-739-769-2
; Sequence 2, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
;  APPLICANT: Monsanto Technology, LLC
;  TITLE OF INVENTION: Methods of Site-Directed Transformation
;  FILE REFERENCE: 38-15(52823)B
;  CURRENT APPLICATION NUMBER: US/10/739,769
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: variant of wild type loxP recombinase site
US-10-739-769-2

  Query Match             100.0%;  Score 34;  DB 19;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.00058;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34


RESULT 6
US-10-448-395-8
; Sequence 8, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
;  APPLICANT: Askew, G. Roger
;  APPLICANT:  Kanki, Kim  L
;  APPLICANT:  Barton, Michael
;  TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
;  TITLE OF INVENTION:  Using an Inducible Gene Silencer
;  FILE REFERENCE: 01997.026400
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; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-8

Query Match 100.0%; Score 34; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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Db 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 7
US-10-448-395-14/c
; Sequence 14, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; TITLE OF INVENTION: Using an Inducible Gene Silencer
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-14

Query Match 100.0%; Score 34; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||||||||
Db 34 ATAACTTCGTATAGCATACATTATACGAACGGTA 1

RESULT 8
US-10-448-395-17/c
; Sequence 17, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; TITLE OF INVENTION: Using an Inducible Gene Silencer
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-448-395-17

Query Match 100.0%; Score 34; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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Db 39 ATAACTTCGTATAGCATACATTATACGAACGGTA 6

RESULT 9
US-10-448-395-18
; Sequence 18, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; TITLE OF INVENTION: Using an Inducible Gene Silencer
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-448-395-18

Query Match 100.0%; Score 34; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||||||||
Db 6 ATAACTTCGTATAGCATACATTATACGAACGGTA 39

RESULT 10
US-10-214-722-14
; Sequence 14, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombinase-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 66 with flanks
US-10-214-722-14

Query Match 100.0%; Score 34; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db          6 ATAACTTCGTATAGCATACATTATACGAACGGTA 39


RESULT 11
US-10-214-722-12/c
; Sequence 12, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
;  APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
;  TITLE OF INVENTION: The use of mutated recognition sequences for multiple
;  TITLE OF INVENTION:  consecutive recombinase-mediated recombinations
;  TITLE OF INVENTION:  in a genetic system
;  FILE REFERENCE: P14567
;  CURRENT APPLICATION NUMBER: US/10/214,722
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: DE 101 40 030.6
;  PRIOR FILING DATE: 2001-08-16
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 67
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-214-722-12

  Query Match            100.0%;  Score 34;  DB 14;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 0.00065;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         43 ATAACTTCGTATAGCATACATTATACGAACGGTA 10


RESULT 12
US-10-916-082-10/c
; Sequence 10, Application US/10916082
; Publication No. US20050153392A1
; GENERAL INFORMATION:
;  APPLICANT: Buelow, Roland
;  APPLICANT:  van Schooten, Wim
;  TITLE OF INVENTION: Improved Transgenesis with Humanized
;  TITLE OF INVENTION:  Immunoglobulin Loci
;  FILE REFERENCE: 39691-0008
;  CURRENT APPLICATION NUMBER: US/10/916,082
;  CURRENT FILING DATE:  2004-08-10
;  PRIOR APPLICATION NUMBER: 60/494,30
;  PRIOR FILING DATE: 2003-08-11
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 75
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-916-082-10

  Query Match            100.0%;  Score 34;  DB 22;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 0.00067;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         50 ATAACTTCGTATAGCATACATTATACGAACGGTA 17


RESULT 13
US-10-118-231-10
; Sequence 10, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
;  APPLICANT: Bigger, Brian W
;  APPLICANT:  Tolmachov, Oleg
;  APPLICANT:  Coutelle, Charles
;  TITLE OF INVENTION: Methods
;  FILE REFERENCE: 102286.141US
;  CURRENT APPLICATION NUMBER: US/10/118,231
;  CURRENT FILING DATE:  2002-04-09
;  PRIOR APPLICATION NUMBER: US 60/327,029
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: GB 0108968.9
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 94
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-118-231-10

  Query Match            100.0%;  Score 34;  DB 14;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 0.00069;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         10 ATAACTTCGTATAGCATACATTATACGAACGGTA 43


RESULT 14
US-10-118-231-16
; Sequence 16, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
;  APPLICANT: Bigger, Brian W
;  APPLICANT:  Tolmachov, Oleg
;  APPLICANT:  Coutelle, Charles
;  TITLE OF INVENTION: Methods
;  FILE REFERENCE: 102286.141US
;  CURRENT APPLICATION NUMBER: US/10/118,231
;  CURRENT FILING DATE:  2002-04-09
;  PRIOR APPLICATION NUMBER: US 60/327,029
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: GB 0108968.9
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 94
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-118-231-16

  Query Match            100.0%;  Score 34;  DB 14;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 0.00069;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||||||
Db         10 ATAACTTCGTATAGCATACATTATACGAACGGTA 43


RESULT 15
US-10-916-082-12/c
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; Sequence 12, Application US/10916082
; Publication No. US20050153392A1
; GENERAL INFORMATION:
;  APPLICANT: Buelow, Roland
;  APPLICANT:  van Schooten, Wim
;  TITLE OF INVENTION: Improved Transgenesis with Humanized
;  TITLE OF INVENTION:  Immunoglobulin Loci
;  FILE REFERENCE: 39691-0008
;  CURRENT APPLICATION NUMBER: US/10/916,082
;  CURRENT FILING DATE:  2004-08-10
;  PRIOR APPLICATION NUMBER: 60/494,30
;  PRIOR FILING DATE: 2003-08-11
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 102
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-916-082-12

  Query Match             100.0%;  Score 34;  DB 22;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 0.0007;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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Db         84 ATAACTTCGTATAGCATACATTATACGAACGGTA 51


Search completed: September  8, 2005, 23:04:40
Job time : 310 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 22:19:49 ; Search time 1585.5 Seconds
(without alignments)
816.263 Million cell updates/sec

Title: US-10-030-658B-16
Perfect score: 34
Sequence: 1 ataacttcgtatagcatacattatacgaacggta 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31.4	92.4	126	2	BF243776	BF243776 601877514
2	31.4	92.4	530	7	CF978786	CF978786 2-14-F03.
3	31	91.2	747	7	CF976774	CF976774 2-12-E11.
4	30.8	90.6	77	2	BF382292	BF382292 601815207
5	30.8	90.6	85	2	BF132923	BF132923 601646101
6	30.8	90.6	88	2	BF246996	BF246996 601854389
7	30.8	90.6	92	2	BF238541	BF238541 601904868
8	30.8	90.6	94	2	BF239393	BF239393 601906694
9	30.8	90.6	97	2	BF243354	BF243354 601878528
10	30.8	90.6	98	2	BF241277	BF241277 601878794
11	30.8	90.6	99	2	BF244775	BF244775 601864535
12	30.8	90.6	100	2	BF209290	BF209290 601872506
13	30.8	90.6	100	2	BF213664	BF213664 601847504
14	30.8	90.6	102	2	BF687672	BF687672 602066704
15	30.8	90.6	106	2	BF244968	BF244968 601864380
16	30.8	90.6	108	2	BF240116	BF240116 601905618
17	30.8	90.6	124	2	BF214305	BF214305 601848531
18	30.8	90.6	130	2	BF674203	BF674203 602136932
19	30.8	90.6	132	4	BF977130	BF977130 602146859
20	30.8	90.6	134	2	BF571954	BF571954 602078272
21	30.8	90.6	135	2	BF214021	BF214021 601847936
22	30.8	90.6	142	2	BF247576	BF247576 601858626
23	30.8	90.6	142	2	BF541761	BF541761 602068101
24	30.8	90.6	144	2	BF674320	BF674320 602137061
25	30.8	90.6	145	2	BF213890	BF213890 601848120
26	30.8	90.6	147	2	BF245810	BF245810 601864716
27	30.8	90.6	149	2	BF244784	BF244784 601864548
28	30.8	90.6	152	2	BF573591	BF573591 602077358
29	30.8	90.6	161	2	BF243567	BF243567 601879377
30	30.8	90.6	166	4	BF977946	BF977946 602148418
31	30.8	90.6	169	2	BF208812	BF208812 601872302
32	30.8	90.6	177	4	BF977761	BF977761 602148383
33	30.8	90.6	268	7	CF978843	CF978843 2-32-G09.
34	30.8	90.6	275	7	CF979148	CF979148 2-18-E07.
35	30.8	90.6	282	7	CF978512	CF978512 2-27-F05.
36	30.8	90.6	320	7	CF978536	CF978536 2-25-E12.
37	30.8	90.6	368	7	CF977378	CF977378 2-25-C02.
38	30.8	90.6	374	7	CF978446	CF978446 2-25-E06.
39	30.8	90.6	431	7	CF978592	CF978592 2-98-D02.
40	30.8	90.6	451	2	BF211083	BF211083 601872840
41	30.8	90.6	455	7	CF978658	CF978658 2-32-F03.
42	30.8	90.6	481	4	BG485698	BG485698 602502544
43	30.8	90.6	524	7	CF978902	CF978902 2-26-H12.
c 44	30.8	90.6	535	8	AQ060250	AQ060250 CIT-HSP-2
45	30.8	90.6	623	2	BF573795	BF573795 602079494

ALIGNMENTS

RESULT 1
BF243776
LOCUS BF243776 126 bp mRNA linear EST 14-NOV-2000
DEFINITION 601877514F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105874 5', mRNA sequence.
ACCESSION BF243776
VERSION BF243776.1 GI:11157706
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 126)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM984 row: 1 column: 03
High quality sequence start: 43
High quality sequence stop: 126.
FEATURES Location/Qualifiers
source 1. .126
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4105874"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length

clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN

Query Match 92.4%; Score 31.4; DB 2; Length 126;
Best Local Similarity 94.1%; Pred. No. 0.011;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||| | ||
Db 84 ATAACTTCGTATAGCATACATTATACGAAGTTA 117

RESULT 2
CF978786
LOCUS CF978786 530 bp mRNA linear EST 24-JUN-2004
DEFINITION 2-14-F03.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA sequence.
ACCESSION CF978786
VERSION CF978786.1 GI:49174244
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 530)
AUTHORS Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
TITLE Gene Expression Profiling of Highly Purified Rat Retinal Ganglion Cells
JOURNAL Unpublished (2003)
COMMENT Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5230
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.
FEATURES Location/Qualifiers
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="Retinal Ganglion Cells"
/lab_host="DH10B"
/clone_lib="Rat retinal ganglion cell"
/note="Organ: Eye; Vector: pDNR-LIB; Site_1: SfiI; Site_2: SfiI; The library was constructed from purified rat retinal ganglion cells. The Creator SMART cDNA Library method (Clontech) was used. EST analysis was performed on the unamplified, non-normalized, non-subtracted library."
ORIGIN

Query Match 92.4%; Score 31.4; DB 7; Length 530;
Best Local Similarity 94.1%; Pred. No. 0.012;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||| | ||
Db 13 ATAACTTCGTATAGCATACATTATACGAAGTTA 46

RESULT 3
CF976774
LOCUS CF976774 747 bp mRNA linear EST 24-JUN-2004
DEFINITION 2-12-E11.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA sequence.
ACCESSION CF976774
VERSION CF976774.1 GI:49172232
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 747)
AUTHORS Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
TITLE Gene Expression Profiling of Highly Purified Rat Retinal Ganglion Cells
JOURNAL Unpublished (2003)
COMMENT Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5230
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.
FEATURES Location/Qualifiers
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="Retinal Ganglion Cells"
/lab_host="DH10B"
/clone_lib="Rat retinal ganglion cell"
/note="Organ: Eye; Vector: pDNR-LIB; Site_1: SfiI; Site_2: SfiI; The library was constructed from purified rat retinal ganglion cells. The Creator SMART cDNA Library method (Clontech) was used. EST analysis was performed on the unamplified, non-normalized, non-subtracted library."
ORIGIN

Query Match 91.2%; Score 31; DB 7; Length 747;
Best Local Similarity 93.9%; Pred. No. 0.018;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGT 33
||||||||||||||||||||||||||||| ||
Db 14 ATAACTTCGTATAGCATACATTATACGAANNGT 46

RESULT 4
BF382292
LOCUS BF382292 77 bp mRNA linear EST 27-NOV-2000
DEFINITION 601815207F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049448 5', mRNA sequence.
ACCESSION BF382292
VERSION BF382292.1 GI:11363595
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 77)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM881 row: m column: 01
High quality sequence start: 6
High quality sequence stop: 77.
FEATURES Location/Qualifiers
source 1. .77
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:4049448"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_56"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 90.6%; Score 30.8; DB 2; Length 77;
Best Local Similarity 94.1%; Pred. No. 0.018;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||| | ||
Db 24 ATAACTTCGTATAGCATACATTATACGAAGGTTA 57

RESULT 5
BF132923
LOCUS BF132923 85 bp mRNA linear EST 24-OCT-2000
DEFINITION 601646101F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4101792 5', mRNA sequence.
ACCESSION BF132923
VERSION BF132923.1 GI:10971963
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 85)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM974 row: b column: 01
High quality sequence start: 12
High quality sequence stop: 85.
FEATURES Location/Qualifiers
source 1. .85
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4101792"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_59"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 90.6%; Score 30.8; DB 2; Length 85;
Best Local Similarity 94.1%; Pred. No. 0.018;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||| | ||
Db 52 ATAACTTCGTATAGCATACATTATACGAAGGTTA 85

RESULT 6
BF246996
LOCUS BF246996 88 bp mRNA linear EST 14-NOV-2000
DEFINITION 601854389F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074143 5', mRNA sequence.
ACCESSION BF246996
VERSION BF246996.1 GI:11161950
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 88)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM924 row: a column: 24
High quality sequence start: 19
High quality sequence stop: 88.
FEATURES Location/Qualifiers
source 1. .88
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4074143"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 90.6%; Score 30.8; DB 2; Length 88;
Best Local Similarity 94.1%; Pred. No. 0.018;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||| | ||
Db 35 ATAACTTCGTATAGCATACATTATACGAAGGTTA 68

RESULT 7

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BF238541
LOCUS       BF238541                  92 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  601904868F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132673 5',
            mRNA sequence.
ACCESSION   BF238541
VERSION     BF238541.1  GI:11152461
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 92)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1032  row: h  column: 18
            High quality sequence start: 10
            High quality sequence stop: 92.
FEATURES             Location/Qualifiers
     source          1. .92
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4132673"
                     /tissue_type="from chronic myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_54"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.75 kb (range 0.9-4.0 kb).  15/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 2;  Length 92;
  Best Local Similarity   94.1%;  Pred. No. 0.018;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              |||||||||||||||||||||||||||| | ||
Db         50 ATAACTTCGTATAGCATACATTATACGAAGGTTA 83


RESULT 8
BF239393
LOCUS       BF239393                  94 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  601906694F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134670 5',
            mRNA sequence.
ACCESSION   BF239393
VERSION     BF239393.1  GI:11153419
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 94)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1037  row: k  column: 23
            High quality sequence start: 25
            High quality sequence stop: 94.
FEATURES             Location/Qualifiers
     source          1. .94
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4134670"
                     /tissue_type="from chronic myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_54"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.75 kb (range 0.9-4.0 kb).  15/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 2;  Length 94;
  Best Local Similarity   94.1%;  Pred. No. 0.019;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              |||||||||||||||||||||||||||| | ||
Db         41 ATAACTTCGTATAGCATACATTATACGAAGGTTA 74


RESULT 9
BF243354
LOCUS       BF243354                  97 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  601878528F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107295 5',
            mRNA sequence.
ACCESSION   BF243354
VERSION     BF243354.1  GI:11157283
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 97)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM988  row: g  column: 08
            High quality sequence start: 17
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            High quality sequence stop: 97.
FEATURES             Location/Qualifiers
     source          1. .97
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4107295"
                     /tissue_type="from acute myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_55"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.65 kb (range 0.9-4.0 kb).  14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 2;  Length 97;
  Best Local Similarity   94.1%;  Pred. No. 0.019;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              |||||||||||||||||||||||||||||| | ||
Db         55 ATAACTTCGTATAGCATACATTATACGAAGGTTA 88


RESULT 10
BF241277
LOCUS       BF241277                98 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  601878794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107430 5',
            mRNA sequence.
ACCESSION   BF241277
VERSION     BF241277.1  GI:11155202
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 98)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM988  row: 1  column: 23
            High quality sequence start: 14
            High quality sequence stop: 98.
FEATURES             Location/Qualifiers
     source          1. .98
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4107430"
                     /tissue_type="from acute myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_55"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.65 kb (range 0.9-4.0 kb).  14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 2;  Length 98;
  Best Local Similarity   94.1%;  Pred. No. 0.019;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              |||||||||||||||||||||||||||||| | ||
Db         56 ATAACTTCGTATAGCATACATTATACGAAGGTTA 89


RESULT 11
BF244775
LOCUS       BF244775                99 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  601864535F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4082696 5',
            mRNA sequence.
ACCESSION   BF244775
VERSION     BF244775.1  GI:11158706
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM946  row: f  column: 09
            High quality sequence start: 13
            High quality sequence stop: 99.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4082696"
                     /tissue_type="glioblastoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_57"
                     /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).   Average
                     insert size 1.55 kb (range 0.9-4.0 kb).  12/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 2;  Length 99;
  Best Local Similarity   94.1%;  Pred. No. 0.019;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||| | ||
Db         57 ATAACTTCGTATAGCATACATTATACGAAGGTTA 90


RESULT 12
BF209290
LOCUS       BF209290                100 bp    mRNA    linear   EST 06-NOV-2000
DEFINITION  601872506F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4096633 5',
            mRNA sequence.
ACCESSION   BF209290
VERSION     BF209290.1  GI:11102876
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM960  row: k  column: 02
            High quality sequence start: 9
            High quality sequence stop: 100.
FEATURES             Location/Qualifiers
     source          1. .100
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4096633"
                     /tissue_type="from chronic myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_54"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.75 kb (range 0.9-4.0 kb).  15/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 2;  Length 100;
  Best Local Similarity   94.1%;  Pred. No. 0.019;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||| | ||
Db         47 ATAACTTCGTATAGCATACATTATACGAAGGTTA 80


RESULT 13
BF213664
LOCUS       BF213664                100 bp    mRNA    linear   EST 06-NOV-2000
DEFINITION  601847504F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078489 5',
            mRNA sequence.
ACCESSION   BF213664
VERSION     BF213664.1  GI:11107250
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM935  row: g  column: 02
            High quality sequence start: 6
            High quality sequence stop: 100.
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4078489"
                     /tissue_type="from acute myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_55"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.65 kb (range 0.9-4.0 kb).  14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             90.6%;  Score 30.8;  DB 2;  Length 100;
  Best Local Similarity   94.1%;  Pred. No. 0.019;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
              ||||||||||||||||||||||||||||||| | ||
Db         47 ATAACTTCGTATAGCATACATTATACGAAGGTTA 80


RESULT 14
BF687672
LOCUS       BF687672                102 bp    mRNA    linear   EST 22-DEC-2000
DEFINITION  602066704F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065817 5',
            mRNA sequence.
ACCESSION   BF687672
VERSION     BF687672.1  GI:11973080
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 102)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM902 row: g column: 02
High quality sequence start: 12
High quality sequence stop: 102.

FEATURES Location/Qualifiers
source 1. .102
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4065817"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 90.6%; Score 30.8; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 0.019;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
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Db 49 ATAACTTCGTATAGCATACATTATACGAAGGTTA 82

RESULT 15
BF244968
LOCUS BF244968 106 bp mRNA linear EST 14-NOV-2000
DEFINITION 601864380F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4082923 5', mRNA sequence.
ACCESSION BF244968
VERSION BF244968.1 GI:11158900
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 106)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM946 row: o column: 20
High quality sequence start: 10
High quality sequence stop: 106.

FEATURES Location/Qualifiers
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/clone="IMAGE:4082923"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 90.6%; Score 30.8; DB 2; Length 106;
Best Local Similarity 94.1%; Pred. No. 0.019;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
||||||||||||||||||||||||||||| | ||
Db 53 ATAACTTCGTATAGCATACATTATACGAAGGTTA 86

Search completed: September 9, 2005, 00:32:15
Job time : 1587.5 secs

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